Sequence 7660, Ap Sequence 8211, Ap Sequence 3786, Ap

Sequence 1371, Apple Sequence 321, Apple Sequence 4, Appli Sequence 1214, Apple Sequence 22, Appli Sequence 59752, Apple Sequence 18, Apple Sequence 18, Apple Sequence 20, Appli Sequence 29, Appli Sequence 39, Appli Sequence 31, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli

4 US-10-128-714-8211 5 US-10-128-714-8211 5 US-10-395-467-1371 6 US-10-395-467-1371 7 US-10-395-467-1371 8 US-10-128-714-3211 9 US-10-369-493-314 10 US-10-425-114-42571 2 US-10-425-114-63907 2 US-10-425-114-63907 2 US-10-425-114-63907 2 US-10-425-114-63907 2 US-10-425-114-63907 2 US-10-426-114-63907 3 US-10-224-880C-18 5 US-10-224-880C-18 8 US-09-817-774-29 US-09-817-774-29 US-09-817-774-45 9 US-10-369-493-2173 10 US-08-879-3137-6 10 US-09-817-774-45 10 US-09-817-774-31

637 644448 646468 6467 646

Sequence 31, Appl Sequence 3263, Ap Sequence 32, Appl

Sequence 43, Appl Sequence 41, Appl

US-09-817-774-43 US-09-817-774-41

ALIGNMENTS

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US-10-425-114-66797
June 14, 2004, 14:40:51; Search time 21.4538 Seconds (without alignments) 1838.444 Million cell updates/sec
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                                                                                                                                     US-10-069-427-6.
755
1 PRVRKNKVELSLLSGLANLC......REIWAEYCKLVPWRILPYVY 140
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2. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
3. (cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3. (cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5. (cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6. (cgn2_6/ptodata/2/pubpaa/NEONB_PUBCOMB.pep:*
7. (cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
10. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
11. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
12. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
13. (cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
14. (cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
15. (cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
16. (cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
16. (cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
17. (cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
18. (cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
19. (cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
19. (cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19. (cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19. (cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum DB seq
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Publication No. US20040034888A1
| Publication No. US2004003488BA1
| Publication No. US2004003488BA1
| Publication No. US2004003488BA1
| APPLICANT: Liu, Jingdong | APPLICANT: Liu, Jingdong | APPLICANT: Liu, Jingdong | APPLICANT: Liu, Jingdong | APPLICANT: Chou, Yihua | APPLICANT: Rovel K | APPLICANT: Tabaska, Jack E | APPLICANT: Cao, Yongwein | TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With | TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement | TITLE OF INVENTION: NUMBER. US/10/425,114 | CURRENT APPLICATION NUMBER. US/10/3-04-28 | NUMBER OF SEQ ID NOS: 734-28 | NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 96.4%; Score 728; DB 12; Best Local Similarity 98.5%; Pred. No. 1.9e-75; Matches 134; Conservative 2; Mismatches 0;
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Sequence 66797, A Sequence 2, Appli Sequence 275960, Sequence 252, App Sequence 9, Appli Sequence 9, Appli Sequence 25, Appli Sequence 25, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 26, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli

12 US-10-425 114-66797 8 US-08-879-137-2 12 US-10-424-596-275560 12 US-10-425-114-58147 16 US-10-648-593-252 8 US-08-879-137-9 8 US-08-879-137-9 8 US-08-879-137-5 9 US-09-817-774-25 9 US-09-817-774-25 9 US-09-817-774-26 9 US-09-817-774-26 9 US-09-817-774-26 9 US-09-817-774-26 9 US-09-817-774-26 9 US-09-817-774-26

208 4002 4

111111 1284100874321

Description

Query Match Length

Result

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113 EARCSOKYREIWAEYCKLVPWRILPYVY 140
                                                    63 BARCAEKYREIWAEYRKLVPWRILPYVY 90
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Publication No. US20040106132A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 REIWAEYCKLVPWRILPYVY 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Oryza sativa
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US-10-648-593-252
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ORGANISM:
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Sequence 275560, Application US/10424599

Sublication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL Showed A APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 GIARHCHYLGDLMLALSFSLPCGISSPVPYFYPIYLLILLIWRERRDEVRCAEKYKEIWA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 NKVELSLLSGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVVGGKLLASGYW 65
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APPLICANT: Sheen, Jen
APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILER REPERENCEN: 00766/338001
CURRENT APPLICATION NUMBER: US/08/879,337A
CURRENT RILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 60/022,086
EARLIER PILICATION NUMBER: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 79.7%; Score 602; DB 8; Length 368; Best Local Similarity 79.1%; Pred. No. 6.9e-61; Matches 106; Conservative 15; Mismatches 13; Indels
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57.1%; Score 431; DB 12; Length 90
Best Local Similarity 86.4%; Pred. No. 7.2e-42;
Matches 76; Conservative 7; Mismatches 5; Indels
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US-10-424-599-275960
                                                                                                                                                                                                                          Sequence 2, Application US/08879337A, Publication No. US20030126630A1, GENERAL INFORMATION:
357 AEYCKLVPWRILPYLY 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT CRGANISM: Arabidopsis thaliana US-08-879-337-2
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ORGANISM: Glycine max
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TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS CURRENT APPLICATION NUMBER: 103/0648, 593
CURRENT APPLICATION NUMBER: 2003-08-26
PRIOR PILING DATE: 2003-08-27
NUMBER: OF SEQ ID NOS: 557
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 252
LENGHRH: 418
Sequence 58147, Application US/10425114
; Sequence 58147, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Enou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Goo, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Nucleic Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Nucleic Acid Molecules Acid Molecules Associated With
; MUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLLVLRERRDEARÇSQKY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Clone ID: UC-OSROM2020008A09_FLI.pep
US-10-425-114-58147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
48.5%; Score 366; DB 16;
Best Local Similarity 54.8%; Pred. No. 1.5e-33;
Matches 69; Conservative 20; Mismatches 33;
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Gaps

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64 YWGIARHCNYLGDLDLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDBARCSQKYREI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 WGIARHCNYLGDILLIALSFSLPCGVSSVVPYFYPTYLLILIVLRERRDEARCSOKYREIW 124
                                                                                                                                                                                                      16 LANLCIF--LIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVV-------GGKLLASGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 VELSLISGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVV----GGKLLASG
                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-08-979-337-5
| Sequence 5, Application US/08879337A
| Sequence 5, Application US/08879337A
| Publication No. US20030126630A1
| GENERAL INPORMATION:
| APPLICANT: Sheen, Jen
| TILE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
| FILE REFERENCE: 00786/338001
| CURRENT APPLICATION NUMBER: US/08/879,337A
| CURRENT PILING DATE: 1997-06-20
| EARLIER APPLICATION NUMBER: 60/022,086
| EARLIER FILING DATE: 1996-06-21
| NUMBER OF SEQ ID NOS: 24
| SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 8; Length 424;
                               DB 8; Length 615;
                                                                                                   Indels
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                                                                                                   31;
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48.9%; Pred. No. 1e-30;
tive 22; Mismatches 43;
                               46.0%; Score 347.5; DB 8
48.5%; Pred. No. 3.3e-31;
iive 22; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25, Application US/0981774
Fatent No. US2020120111A1
GENERAL INFORMATION:
APPLICANT: CHOE, Sunghwa
TITLE OF INVENTION: DAÉS WITANTE
FILE REFERENCE: 2225-0020 / 91020.002
CURRENT FILING DATE: 2020-03.26
FRIOR PELICATION NUMBER: US/09/817,774
CURRENT FILING DATE: 2000-03.26
FRIOR PILING DATE: 2000-03.26
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patentin Ver. 2.0
SSOID NO. 25
LENGTH: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                     125 AEYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    600 EKYCQRVPYŘÍFPYIÝ 615
                            Query Match
Best Local Similarity 48.5%
Matches 66; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67; Conservative
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Best Local Similarity
Matches 67; Conserv
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US-09-817-774-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 WGFVRHPNYLGDLIMALAWGLPCGFNHILPYFYIIYFTMLLVHRBARDEYHCKKKYGVAM 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LANLCIF--LIGYLVFRGANKQXHVFKKDPKAPIWGKPPKVV------GGKLLASGY 64
LCIF-LIGYLVFRGANKQKHVFKKDPKAP-IWGKP--PKVVGGKLLASGYWGIARHCNYL
                                      17; Gaps
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APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/879,337A
CURRENT APPLICATION NUMBER: 06/022,086
EARLIER PILING DATE: 1999-06-20
EARLIER PILING DATE: 1996-06-21
NUMBER OF, SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 9
LENGTH: 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: US-09-817-774-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
46.0%; Score 347.5; DB 9;
Best Local Similarity 48.5%; Pred. No. 2.1e-31;
Matches 66; Conservative 22; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQUENCE 22, Application US/0981774
Patent No. US20020120111A1
GENERAL INFORMATION:
APPLICANT: CHOE, SUNGHWA
APPLICANT: CHOE, SUNGHWA
TITLE OF INVENTION: DWÉS MUTANTS
FILE REFERENCE: 2225-0020 / 91020.002
CURRENT APPLICATION NUMBER: US/09/817,774
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 06/192,202
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ 1D NOS: 45
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 AEYCKLVPWRILPYVY 140
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411 EKYCQRVPYRIFPYIY 426
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US-08-879-337-9
                                                                                                                                                                                                                                                                  135 ILPYVY 140
                                                                                                                                                                                                                                                                                                                                  413 IMPYIY 418
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-09-817-774-22
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US-08-879-337-9
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Gaps

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Gaps

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EVARS, Cheryl

LALICANT: Merberg, David

APPLICANT: Treacy, Munice

APPLICANT: Treacy, Munice

APPLICANT: Steininger II, Robert J.

APPLICANT: Steininger II, Robert J.

APPLICANT: Steininger II, Robert J.

APPLICANT: Gordon G.

APPLICANT: Steininger II, Robert J.

APPLICANT: Steininger II, Robert J.

APPLICANT: Steininger II, Robert J.

APPLICANT: Gordon G.

APPLICANT: Gordon G.

APPLICANT: Gordon G.

APPLICANT: Gordon G.

APPLICANT: Gordon SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

FILE REFERENCE: 6055-64X

CURRENT APPLICATION NUMBER: US/09/729,674

CURRENT FILING DATE: 2000-12-04

PRIOR PILING DATE: 2000-13-30

NUMBER OF SEQ ID NOS: 283

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 142

LENGTH: 475

TYPE: PD"
                                                                                                                                                                                                                                                                                                                                                                                                                                              76 DLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIWAEYCKLVPWRI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 -GGKLLASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEA 114
                                                                                                                                                                                                                                                                                                                                                                                                                  19 LCIFLIGYLVFRGANKOKHVFKK---DPKAPIWGKPPKVVGGKLLASGYWGIARHCNYLG
                                                                                                                                                                                                                                              , OTHER INFORMATION: Description of Artificial Sequence: LBR-RAT
US-09-817-774-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 VELSLLSGLANLCIFLIGYLVFRGANKOKHVFKK-DPKAPIWGKPPKVV----
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                                                                                                                                                                                                                                                                                                                                                                         40; Indels
                                                                                                                                                                                                                                                                                                                         y Match 43.9%; Score 331.5; DB 9. Local Similarity 48.8%; Pred. No. 1.5e-29; nes 61; Conservative 21; Mismatches 40.
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CURRENT APPLICATION NUMBER: US/09/817,774
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/192,202
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 23
LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 142, Application US/09729674 Patent No. US20010039335A1
                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                         61; Conservative
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US-09-729-674-142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 LPYVY 140
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Best Local S
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Matches
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PLILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 22601
LENGTH: 424
                                                                                                                                                                                                                                                                                                                                                        64 YWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREI 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 YWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREI 123
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                                                                                                                                                                                                                                       8 VELSLLSGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVV----GGKLLASG
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                                                                                                                                              Length 424;
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                                                                                                                                         Query Match 45.2%; Score 341.5; DB 9; Length Best Local Similarity 48.9%; Pred. No. 1e-30; Matches 67; Conservative 22; Mismatches 43; Indels
                                                                          ) OTHER INFORMATION: Description of Artificial Sequence: US-09-817-774-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 22601, Application US/10369493; Publication No. US20030233675A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09817774
Patent No. US20020120111A1
GENERAL INCRMATION:
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN A., Kenneth
TITLE OF INVENTION: DWE5 MUTANTS
FILE REFERENCE: 2225-0020 / 91020.002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Schizosaccharomyces pombe
                                                                                                                                                                                                                                                                                                                                                                                                                         124 WAEYCKLVPWRILPYVY 140
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408 WEKYCKAVKYRIIPYVY 424
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WEKYCKAVKYRIIPYVY 424
                               ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.3%; Score 319.5; DB 9; Length 475;
43.2%; Pred. No. 4.2e-28;
live 26; Mismatches 44; Indels 13
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is gequence 32, Application US/10429160

sequence 32, Application US/10429160

publication No. US20040023276A1

is GRNERAL INFORMATION:

APPLICANT: Ward, Teresa R

APPLICANT: Linsley, Peter S

CURRENT FILENGATION UNMER: US/10/429,160

CURRENT APPLICATION NUMBER: US 60/377,714

PRIOR APPLICATION NUMBER: US 60/377,714

PRIOR APPLICATION NUMBER: US 60/377,714

SOFTWARE: PatentIn version 3.1

SOFTWARE: PatentIn version 3.1

SEQ ID NO 32

LENGTH . 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: Description of Artificial Sequence: US-09-817-774-26
                                                                                                                                                                                     Sequence 26, Application US/09817774
Patent No. US20020120111A1
GENERAL INFORMATION
PAPLICANT: CHOE, Sunghwa
APPLICANT: CHOE, Sunghwa
TITLE OF INVENTION: DAFF MUTANTS
FILE REFERENCE: 2225-0020 / 91020.002
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US/09/817,774
PRIOR PILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 45
SEQ PRIOR PLING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 26
LENGTH: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 RCSQKYREIWAEYCKLVPWRILPYVY 140
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                                                          115 RCSQKYREIWAEYCKLVPWRILPYVY 140
                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 43.2*
Matches 63; Conservative
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CORGANISM: Homo sapiens
US-10-429-160-32
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US-09-817-774-26
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42.3%;

Query Match Best Local Similarity

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390 HHSKLLVSGFWGVARHFNYVGDLMGSLAYCLACGGGHLLPYFYIIYMAILLTHRCLRDEH 449
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                                                                56 -GGKLLASGYWGIARHCNYLGDILLALSFSIPCGVSSVVPYFYPTYLLILLVLRERRDEA 114
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                                        8 VELSLLSGLANLCIFLIGYLVFRGANKOKHVFKK-DPKAPIWGKPPKVV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence:
US-09-817-774-27
44;
26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Application US/09817774

Batent No. US2020120111A1

GENERAL INFORMATION:
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN A., Kenneth
ITTLE OF INVENTION: DAFS MUTANTS
FILE REPERBNCE: 2225-0020 / 91020.002
CURRENT FILING DATE: 2001-03-26
FRIOR PAPLICATION NUMBER: 60/192,202
PRIOR PAPLICATION NUMBER: 60/192,202
PRIOR PAPLICATION NUMBER: 60/192,202
NUMBER OF SEQ ID NOS: 45
NUMBER OF SEQ ID NOS: 45
SEQ ID NO 274
SEQ ID NO 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 RCSOKYREIWAEYCKLVPWRILPYVY 140
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Best Local Similarity 43.2%
Matches 63; Conservative
  63; Conservative
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Job time
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Sequence 28189, Application US/10425114

| Sequence 28189, Application No. US20040034888A1
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Lit, Jingdong
| APPLICANT: Screen, Steven E
| APPLICANT: Screen, Steven E
| APPLICANT: Tabaska, Jack E
| APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION NUMBER: US/10/425,114
| CURRENT APPLICATION NUMBER: US/10/425,114
| CURRENT PLING DATE: 2003-04-28
| SEQ ID NOS: 73128
| SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 46, Appl
Sequence 1079, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 711, Appl
Sequence 7211, Appl
Sequence 5211, Appl
Sequence 27473, Appl
Sequence 27473, Appl
Sequence 27473, Appl
Sequence 27473, Appl
Sequence 25311, Appl
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                      Sequence 1, Appli
Sequence 10, Appli
Sequence 3, Appli
Sequence 30115, A
Sequence 128, Appli
Sequence 1154, Appli
Sequence 599, Appli
Sequence 599, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 114179, Sequence 134379,
Sequence 134379,
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB4746-067-F5_FLI
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755
1 PRVRKNKVELSLLSGLANLC......REIWAEYCKLVPWRILPYVY 140
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(ggn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
(ggn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
(ggn2_6/ptodata/2/pubpna/USO6_PUBGOMB.seq:*
(ggn2_6/ptodata/2/pubpna/USO6_PUBGOMB.seq:*
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                     nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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Match Length DB
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Database :

Score

Result No.

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Searched:

Scoring table:

Perfect score:

Sequence:

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1026 CCATGTGGGAATAAGTTCTCCGGTTCCATATTTCTACCCGATATACCTTCTGATAATAATATG 1085
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                                                                                                            26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jang, Jyan-Chyun
APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/879,337A
CURRENT APPLICATION NUMBER: 00/022,086
EARLIER APPLICATION WHEEE: 1997-06-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PascSEQ for Windows Version 3.0
LENGTH: 2975
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Matches:
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                            US-10-069-427-6 (1-140) x US-08-879-337-1 (1-1429)
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US-08-879-337-10
Sequence 10, Application US/08879337A; Publication No. US20030126630A1; GENERAL INFORMATION:
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LOCATION: (1) ... (2975)
OTHER INFORMATION: N can be any
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ORGANISM: Arabidopsis thaliana
FEATURE:
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496.00
44.49%
39.34%
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Query Match:
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                                                                                                                                                                                                                         GlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08879337A

Sequence 1, Application US/08879337A

Publication No. US2000126630A1

GENERAL INFORMATION:

APPLICANT: Jang, Jyan-Chyun

APPLICANT: Sheen, Jen

TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF

TITLE OF INVENTION: PLANT STEROL

CURRENT APPLICATION NUMBER: US/08/879,337A

CURRENT FILING DATE: 1997-06-20

BARLIER APPLICATION NUMBER: 60/022,086

BARLIER FILING DATE: 1996-06-21

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 1

ENTIRE THE SECSEQ FOR Windows Version 3.0

SEQ ID NO 1

ENTIRE THE SECSED FOR WINDOWS VERSION 3.0
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: N can be any nucleotide.
US-08-879-337-1
                                                                                                           Gaps:
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NAME/KEY: variation
                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Query Match:
US-10-425-114-28189
                          Alignment Scores:
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Pred. No.:
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US-08-879-337-1
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us-10-069-427-6.rnpb

TANGTICTGAGACATGGGGGTTATTTCCATTACATATCTACACTAAGAACCCACTA 2126 US-08-879-337-3
Phelly 40 Pred. No.: Score: Score
Title 10 Predict 17 10 Predict 17 10 Predict Predict 10 Predict Predic
Phelity 40 Predict P
Phelity 40 Pred-No. 1.9 Pred-No.
Phelity 40 Prede: No.: 5.17e-58 Length: 6587 107 Score: 5.17e-58 Length: 6587 107 Score: 107 Score: 107 Score: 108
Scores: S.17e-58 Length: 6587
Alignment Scores: S.17e-58 Length: 6587
Alignment Scores: Score: Pred. No.: Score: A14.49\$ Conservative: Best Local Similarity: Query Match: Best Local Similarity: A39.34 Indels: Best Local Similarity: A39.34 Indels: Best Local Similarity: A39.34 Indels: Best Local Similarity: Best Local Similarity: A39.36 AS0.10-069-427-6 (1-140) x US-08-879-337-3 (1-6587) AS10-069-427-6 (1-140) x US-08-
Alignment Scores: 2.17e-58
40 Alignment Scores: 5.17e-58 Length: 6587 Score: 496.00 Matches: 107 Score: Percent Similarity: 44.9\$ Mismatches: 14 Best Local Similarity: 44.9\$ Mismatches: 14 Guery Match: 65.70\$ Mismatches: 137 Ouery Match: 8 Guery Match: 8 Guery Match: 8 Guery Match: 137 Guery Match: 8 Guery Match: 137 Guery Match: 8 Guery Match: 137 Guery Match: 137 Gaps: 3 Gaps: 3 Gaps: 137
40 Alignment Scores: 5.17e-58 Length: 6587 Score: 496.00 Matches: 107 Score: 496.00 Matches: 107 Best Local Similarity: 494.49\$ Conservative: 14 Best Local Similarity: 49.44.9\$ Mismatches: 14 Query Match: 65.70\$ Indels: 137 Gaps: 3 Gaps: 3 Cy 6 AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIle-GI Db 5361 AACAAAGTAGAATTCCTGCGATTGTAGTAGTCTTGTTAGTAGGG Qy 25 y
Alignment Scores: Ered. No.: 2186 Score: 496.00 Matches: 107 Percent Similarity: 44.49\$ Conservative: 14 Query Match: B: 65.70\$ US-10-069-427-6 (1-140) x US-08-879-337-3 (1-6587) Cy 65 S361 Cy 67 CABLE STREET S
40 Alignment Scores: 5.17e-58 Length: Score: 496.00 Matches: Score: 5.07e-58 Length: Application Additional Similarity: 44.49% Conservative: Best Local Similarity: 39.34% Mismatches: Query Match: B: 70% Gaps: B: 2246
40 Alignment Scores: 5.17e-58 Length: 2186 Score: 496.00 Matches: Percent Similarity: 44.49\$ Conservative: 60 Rest Local Similarity: 39.34\$ Mismatches:
Phely 40
Dhoin 40
CCACTA 2126 US-08-879-337-

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; Sequence 128, Application US/10648593; Publication No. US20040106132A1; GENERAL INFORMATION:
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Best Local Similarity:
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Query Match:
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; ORGANISM: Homo :
US-10-648-593-128
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US-10-648-593-128
       Alignment Scores:
Pred. No.:
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US-10-425-114-30215

Sequence 30215, Application US/10425114

Publication No. US20040034888A1

Publication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Abou, Yihua

APPLICANT: Aboulc, David K.

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Pabska, J
                                                                                              and Other Molecules Associated With or Plant Improvement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 ValProTyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgArgAsp 112
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76
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Caro Yongwei
ITILE OF INVENTION: Soy Nucleic Acid Molecules and O
TITLE OF INVENTION: Plants and Uses Thereof for Plant PILE REPERENCE: 38-21(3323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 133118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: UC-OSRCM202008A09_FLI
US-10-425-114-30215
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-424-599-133118
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86.36%
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                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Glycine max
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Best Local Similarity:
Query Match:
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APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
CURRENT APPLICATION NUMBER: US/10/648,593
CURRENT APPLICATION NUMBER: US/406,385
PRIOR FILING DATE: 2002-08-27
NUMBER OF SEQ ID NOS: 557
SOFTWARE: PATHMED AND SECORD ON SECORD ON SECOND ON S
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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1162 CITCTIGITICATAGAAATGCACGGGATGATCACAAATGCCGTGTAAAGTATGGTGAAGAT 1221
                                                                                     1102 TGTTTACCTGCTGGATTTGGTTCACCGATCCCGTACTTTTATGTTGCCTATTTTGGTGTG 1161
1042 TGGTGGGGAATGGCACGCCACATCAACTATTTTGGTGATTGGATTATGGCTTGGGCTTGG 1101
                                                    84 SerieuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuIle 103
                                                                                                                                                                 LeuLeuValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIle 123
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APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Mack, David H.
APPLICANT: Mack, David H.
APPLICANT: Wateron, Susan R.
APPLICANT: Wateron, Susan R.
APPLICANT: Eos Biotechnology, Inc.
ITLE OF INVENTION: Methods of Diagnosis of Cancer
ITLE OF INVENTION: Methods of Screening for Modulators of Cancer
ITLE OF INVENTION: Methods of Screening for Modulators of Cancer
ITLE OF INVENTION: Moder: US /10/295,027
CURRENT APPLICATION NUMBER: US 60/350,666
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR PLING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR PLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR PLING DATE: 2002-01-08
PRIOR PL
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                                                                                                                                                                                                                                                                       124 TrpAlaGluTyrCysLysLeuValProTrpArglleLeuProTyrValTyr 140
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NUMBER OF SEQ ID NOS: 1386
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1154
LENGTH: 2100
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Publication No. US20030232350A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Ginsh, Kurt C.
APPLICANT: Glynne, Richard
APPLICANT: Hevezi, Peter A.
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ORGANISM: Homo sapiens
US-10-295-027-1154
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Starer, Steven C.
APPLICANT: Staven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE OF INVENTION: 2003-02-28
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR PLING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                |||----|||----|||
1063 ACTTICCGAAAGAATCCTICTGACCCCAGAGTGGCTGGGGCTTGAGACCATCTCTACAGCC 1122
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                             ValPheLysLysAspProLysAlaPro---IleTrpGlyLysPro-----ProLysVal
                                                                                                                                      55 ValGlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu
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Sequence 46288, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
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US-10-369-493-46288
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LENGTH: 1272
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                          28 ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro 46
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GRGANISM: Homo sapiens
US-10-342-887-599
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1533 ATCTGCCTCATCAATGCTACTGGTTACTACATCTTCCGTGGGGGGGAATTCCCAGAAAAAC 1592
                                                                                1593 ACTITICGGAAGAATCCITCTGACCCCAGAGTGGCTGGGCTTGAGACCATCTCTACAGCC 1652
                                                                                                                                                                                                                                                1773 TACTTCTACCTCCTCTACTTCACCGCGCTGCTGGTGCACCGTGAGGCCCGGGATGAGCG- 1831
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  19 LeuCysIlePhe---LeuIleGlyTyrLeuValPheArgGlyAlaAsnLysGlnLysHis 37
                                                     38 ValpheLysLysAspProLysAlaPro---IleTrpGlyLysPro----ProLysVal
                                                                                                      55 ValGlyGlyLysLeuLeuAlaSerGlyTyTTTTFGlylleAlaArgHisCysAsnTyrLeu
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APPLICANT: Steining' Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Wang, Gardon G.
APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT APPLICATION NUMBER: 099/539,330
PRIOR FILING DATE: 2000-03-30
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Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Spaulding, Vikki
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Patent No. US20010039335A1
GENERAL INFORMATION:
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APPLICANT: McCoy, John M.
PAPLICANT: LaVallie, Edward R.
APPLICANT: Collins Racie, Lisa A.
APPLICANT: Evans, Cheryl
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 141
ELENGTH: 2481
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ORGANISM: Homo sapiens
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1302 ATCTGGGGCAGGAAGCCCAAGGTCATCGAGTGCTCCTACACATCCGCCGACGGGCAGAGG 1361
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1302 ATCTGGGGCAGGAAGCCCAAGGTCATCGAGTGCTCCTACACATCCGCCGACGGGCAGAGG 1361
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                                                                                                                                     ---GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu
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APPLICANT: Ward, Teresa R
APPLICANT: Linsley, Peter S
APPLICANT: Linsley, Peter S
APPLICANT: Linsley, Lund, Lund
TITLE OF INVENTION: LXR Ligand Induced Genes and Proteins
FILE REPREMENT: S000
CURRENT APPLICATION NUMBER: US/10/429,160
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US 60/377,714
PRIOR APPLICATION NUMBER: US 60/377,714
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
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                                                         47 IleTrpGlyLysProProLysValVal------
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1602 CTGCTGCTGGAATCTTC 1619
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ORGANISM: Homo sapiens
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Best Local Similarity:
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US-10-429-160-31
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                                                     1242 ATCTTCCGGGTGGCCAACCACAGAAGGACCTGTTCCGCCGCACGGATGGGCGCTGCCTC 1301
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1302 ATCTGGGGCAGGAAGCCCCAAGGTCATCGAGTGCTCCTACACATCCGCCGACGGCAGAGG 1361
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1542 |GTGGGGCAAGTACGGCCGGAACTGGGAGCGCTACACCGCCGCAGTGCCTTACCGC 1601
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                                                                                                                                                                                                                                                  GlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro 94
                ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro 46
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APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REPERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 599
LENGTH: 2597
                                                                                                                                                                    56 ---GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeu
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Mismatches:
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                                                                                              ileTrpGlyLysProProLysValVal----
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Publication No. US20030224374A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Roberts, Chris
APPLICANT: Roberts, Chris
APPLICANT: Van de Vijver, Marc
APPLICANT: Van de Vijver, Marc
APPLICANT: Bernards, Rene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NM 001360
DATABASE ENTRY DATE: 2001-06-18
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Best Local Similarity:
Query Match:
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US-10-172-118-599
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US-10-172-118-599
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Pred. No.:
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GENERAL INFORMATION:
GENERAL INFORMATION:
INTIE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT FILING DATE: 2002-04-30
FRIOR PELICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02/06
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/198,218
PRIOR APPLICATION NUMBER: US 60/197,363
PRIOR PELING DATE: 1999-110-23
PRIOR PELING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR FILING DATE: 1999-10-24
PRIOR PELING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PELING DATE: 1999-01-28
PRIOR PELING DATE: 1999-00-28
PRIOR PELING DATE: 1999-00-36
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                            GlylleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu
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Matches:
Conservative:
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GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US/02.04-30

PRIOR APPLICATION NUMBER: US/02.04-30

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR PAPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,218

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1099-09-28

PRIOR FILING DATE: 1099-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

NUMBER OF SEC ID NOS: 325720

SOFTWARE: FastEEQ for Windows Version 4.0

LENGTH: 607

LENGTH: 607
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Matches:
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Best Local Similarity:
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US-10-027-632-134379
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US-10-027-632-134379
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Search completed: June 14, 2004, 16:03:04 Job time: 343.411 secs

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BC029171 Mus muscu
BC010051 Mus muscu
BC021516 Mus muscu
AB002466 Rat mRNA
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AX133650 Arabidops
AR277118 Arabidops
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AX162105 Oryza sat
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AX17213 Sequence
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AR27913 Sequence
AR27915 Sequence
AR27915 Sequence
AR27919 Oryza sat
AR177034 Sequence
AF565976 Arabidops
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BC012857 Homo sapi
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BC012857 Homo sapi
AR77634 Sequence
AR035681 Bos tauru
BC012857 Homo sapi
AR174090 Sequence
AR03554 Arabidops
AR53671 Dictyoste
AR03276 Homo sapi
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755
1 PRVRKNKVELSLLSGLANLC.....REIWAEYCKLVPWRILPYVY 140
                                                                                                                           June 14, 2004, 09:48:07; Search time 2238.35 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                        OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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AX107837

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Glycine max (soybean)
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Glycine max
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
rosids, eurosids I, Fabales, Fabaceae; Papilionoideae, Phaseoleae,
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Genes encoding sterol delta-15 reductase in plants
Patent: WO.0123539-A 3 05-APR-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
Location/Qualifiers
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Chromatin associated proteins
Patent: US 6306632-A 3 23-OCT-2001;
Location/Qualifiers
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Sequence 3 from Patent W00123539.
AX107835 AX107835.1 GI:13923232
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                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Patent: WO 0123339-A 5 05-APR-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
Location/Qualifiers
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Sequence 3 from patent US 6306632.
AR174091
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Cahoon, R.E. and Rafalski, J.Antoni.
      AX107837 667 bp
Sequence 5 from Patent W00123539,
AX107837
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Eukaryota; Viridiplantae;
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24 89 44 209

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30-APR-2001

PAT

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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105

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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Osoids; eurosids; Louidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

2. Chases 1 to 1110)
2. Chang, E., Dale, J.M., Goldsmith, A.D., Haysshizaki, Y., Ishida, J., Jones T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, X., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, Y., Arabidopsis ORF clones

4. Unpublished
3. Check, R., Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Ishida, J., Jones T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Ishida, J., Uones T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Ishida, J., Uones T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Ishida, J., Uones T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Ishida, J., Uones T., Yamada, M., Ishida, J., Onodera, C.S., Palm, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Xu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Direct Submission

Blinded to Submission

Nouly M. Lin, J. Waller, M. Wallysis Laboratory, The Salk Institute for Blooglocal Studies, 10010 N. Torrey Pines Road, La Jolla, CS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AY133650 1110 bp mRNA linear PLN 07-AUG-2002 Arabidopsis thaliana AT3g52940/F8J2_111 mRNA, complete cds. AY133650
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                                                                                                                                                                                                                                                                                                                                                                                                 106 ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
                                                                                                                                               886 CCTATCTGGGGTAAGCCTCCAAAAGTCATTGGTGGAAAGCTACTTGCTTCTGGTTATTGG 945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL DUNAs: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Banh, J. Bowser, L., Chan, M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Jones, T.,
                                                                                                                                                                                                                                                                                            86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeulleLeuLeu
                                                                                                                         46 ProlleTrpGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyrTrp
                                                                                                                                                                                                          GlyllehlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu
166 AACAGTGTGGAGTTAACACCAGCTGCCATTGTAGCTAATTGCTTTGTGTTTCCTGATTGGA
                                         26 TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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                                                                                                                                                                                                                                                                            851 TACATGGTATTTCGAGGAGGAAACAAGCAAAAGCATGTGTTCAAAAGAATCCAAAGGCT
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Genes encoding sterol delta-15 reductase in plants
Patent: WO 0123539-A 7 05-APR-2001;
E.I. DU PONT DE NEMOURS AND COMPANY (US)
Location/Qualifiers
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Sequence 7 from Patent WO0123539.
AX107839
                                                                                                                         US-10-069-427-6 (1-140) x AX107835 (1-1631)
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WGKPPVVVGGKLLVSGYWGIARHCNYLGDLMLALSFSLPCGISSPVPYFFILLIL
IWRERRDBVRCAEKYKEIWABYLLVPWRILLPYV"
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                                                                                                       Arabidopsis thaliana Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases: 1 to 1413)
Schrick, K., Mayer, U., Horrichs, A., Kuhnt, C., Bellini, C., Dangl, J., Schmidt, J. and Jurgens, G. aductase required for organized cell division and expansion in Arabidopsis embryogenesis
                                                                                                                                                                                                                                                                                                                           Chases 1 to 1413)
Schrick, K., Mayer, U., Horrichs, A., Kuhnt, C., Bellini, C., Dangl, J., Schnidt, J. and Jurgens, G.
Direct Submission
Submitted (17-APR-2000) ZMBP, University of Tuebingen, Auf der Morgenstelle 1, Tuebingen D-72076, Germany
Location/Qualifiers
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/db_xref="taxon:3702"
                                                                                          Arabidopsis thaliana (thale cress)
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clone="BAC F8J2"
                                                       AF256535.1 GI:8980703
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609.00
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/gene="FK"
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//producid="Arigis480.1"
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MGKPPVVVGGKLLJVGGTAGLAVKTCDLAVALALSFSLPGGISSFVFYFYPITLILL
IWRERRDEVRCAEKYKEIWAEYLRLVPWRILDYY"
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                                                                                    Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers 1.0110
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Ondera,C.S., Pallm,C.J., Quach,H.L., Southwick,A., Tang,C.C.,
Torium,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu,G., Davis,R.W.,
Theologis,A., and Ecker,J.R.
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FYNYGGKLLVSGYYGTARHCNYLGDLMLALGFSLPCGISSSVPYFYPIYLILLIMRE
RRDEVRCAEKYKEINAEYLRLVPWRILLPYVY"
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AF257178 1inear PLN 05-JUL-2000
Arabidopsis thaliana C-14 sterol reductase (FACKEL) mRNA, complete
                                                                                                        Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1429)
Jang, J.C., Fulioka, S., Tasaka, M., Seto, H., Takatsuto, S., Ishii, A.,
Aida, M., Yoshida, S. and Sheen, J.
A critical role of sterols in embryonic patterning and meristem
programming revealed by the fackel mutants of Arabidopsis thaliana
20317032
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                                                                                                                                                                                                                                                                                                                                          Submitted (17-APR-2000) Horticulture and Crop Science, The Ohio State University, 310A Kottman Hall, 2021 Coffey Road, Columbus, 43210, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 TyrLeuValPheArgGlyAlaAsnlysGlnLysHisValPheLysLysAsaspProLysAla
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Jang, J.-C. and Sheen, J.
Direct Submission
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/gene="FACKEL"
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              ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuLeu 105
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1 (bang, J. - C. and Sheen, J.
Plant sterol reductases and uses thereof
Patent: US 6639130-A 2 28-OCT-2003;
Location/Qualifiers
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ELI CDNA, oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae, Bhrhartoideae, Oryzeae, Oryza.
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                              ecotype="Columbia"
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                                             1026 CCATGTGGAATAAGTTCTCCGGTTCCATATTTCTACCCGATATACCTTCTGATACTATTG 1085
                                                                                                                                                                                               Arubaysa
Arabidopsis thaliana AT3g52940/F8J2_111 mRNA, complete cds.
AY064964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicctyledons; core eudiccts; Cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases I to 1449)

Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamita, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Pavis, R., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (30-NOV-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      t
C
   ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeulleLeuLeu 105
                                                                                                                                                     ValleuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
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                                                                                                                                                                                                                                                                                          /organism="Arabidopsis thaliana"
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Arabidopsis cDNA clones Unpublished

(bases 1 to 1449)

TITLE JOURNAL REFERENCE AUTHORS

Direct Submission and Ecker, J.R.

TITLE

COMMENT

FLI CDNA. Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

ORGANISM

REFERENCE AUTHORS

AY064964.1 GI:17473515

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

AY064964

рp

LOCUS

1066

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946

45

1126

85

105

/mol_type="mRNA" /db_xref="taxon:3702"

source

FEATURES

TITLE

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URL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ook,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
FAIS Genome, S., Ishibiki,J., Kawamata,M.,
Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
Masuda,H., Murra,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M.,
Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murzakani,K.
Genome Exploration Research Group in Riken: Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
                             Kikuchi,S., Satch,K., Nagater,T., Kawagashira,N., Dol,K.,
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Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
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Kusumegi,T., Oka,M., Ryu,R., Wodayashi,M., Yaroka,M., Mura,J.,
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Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imcani,K., Shii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Salto,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Sience 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Itda, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishi, Y., Ishikawa, M., Itch, M., Kagawa, I., Kanagawa, S., Katch, H., Kawagashira, N., Kawai, J., Kawanata, M., Katch, H., Kawagashira, N., Kawai, J., Kabayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Musumegi, T., Li, C., Lu, M., Masunca, H., Marsubara, K., Murata, M., Magata, T., Murasaki, R., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ooka, M., Sanoi, M., Sanoi, D., Sato, K., Satoh, K., Satoh, K., Sanoi, M., Sanoi, D., Satoh, K., Satoh, K., Sanoi, M., Sanoi, D., Satoh, K., Satoh, K., Sanoi, M., Sanoi, M., Sanoi, M., Tagami-Takeda, Y., Tagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Tagami-Takeda, Y., Tagawa, A., Shiraki, K., Tagami-Takada, Y., Tagawa, A., Suzuki, Y., Tagami-Takada, Y., Tagawa, A., Suzuki, Y., Tagami-Takada, Y., Tagawa, A., Tarakahashi, F., Takaku-Akahira, S., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A., Tagami, Y., Yasunishi, A., Yazaki, J., Jana, Jaka, Jaka,
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Direct Submission
Submitted (12-SRP-2002) Shoshi Kikuchi, National Institute of
Submitted (12-SRP-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondal, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@mias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
Agrobiological Sciences Rice Full-Length cDNA Project Team:,
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COMMENT

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AF263244 2828 bp DNA linear PLN 13-JUL-2000 Arabidopsis thaliana C-14 sterol reductase gene, complete cds. AF263244
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae, Arabidopsis.
1 (bases 1 to 2828)
Jang,J.C., Fulioka,S., Tasaka,M., Seto,H., Takatsuto,S., Ishii,A.,
Aida,M., Yoshida,S. and Sheen,J.
A critical role of sterols in embryonic patterning and meristem
programming revealed by the fackel mutants of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 LeuProCysGlyVal----SerSerValValProTyrPheTyrProThrTyrLeuLeu 102
               Murata, M.,
Osato, N.,
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Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Catoh, H., Sakai, C., Sako, K., Shibata, K., Satoh, H., Sasaki, D., Saco, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Tasawa, A., Takhashi, F., Takhari, S., Tanaka, T., Toya, T., Maki, K., Yasunishi, A. and Hayashizaki, Y.
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/mol type="mRNA"
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/db xref="txxon:39947"
/clone="002-110-E10"
                                                                                                                                                                                                                                                                                                                                                     1456
112
9
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Matches:
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Mismatches:
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.1176,1287. .1378,
.2338,2486. .2562,
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                                            TTACCTTGGCGACTTGATGCTTGTCCTTCAGCTTTGCCATGTGGAATAAGGTAACT 2488
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Arabidopsis thaliana
Bukaryota, Virialiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

( pases I to 3992)
Schrick, K., Mayer, U., Horrichs, A., Kuhnt, C., Bellini, C., Dangl, J.,
Schmidt, J. and Jurgens, G.
FACKEL is a sterol C-14 reductase required for organized cell
division and expansion in Arabidopsis embryogenesis
Genes Dev. 14 (12), 1471-1484 (2000)
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Schrick, K., Mayer, U., Horrichs, A., Kuhnt, C., Bellini, C., Dangl, J.,
Schmidt, J. and Jurgens, G.
Direct Submission
Submitted (17-APR-2000) ZMBP, University of Tuebingen, Auf der
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| organism="Arabidopsis thaliana" |
| mol_type="genomic DNA" |
| db_xref="taxon:3702" |
| chromosome="3" |
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1221. 1268,1416. 1556,1624. 1670,1762. 1843,1991. 2067,

2144. 2263,1408. 2482,2675. .>2828)

/product="C-14" sterol reductase"

join (84. 131,230. 347,439. 509,622. 678,789. 880,

1221. 1268,1416. 1536,1624. 1670,1762. 1843,1991. 2067,

2144. 2263,2408. 2482,2675. 2828)

/note="FACKEL"

/product="C-14" sterol reductase"

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/product="C-14" sterol reductase"

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SDGSQLRYRCNGLLALILLVAILGICAKLGIVSPLVVADRGLELLSATFIFCVLVTLA
LYVTGRSSSNKGSSLKPHVSGNLVHDWWFGIQLNPQFMSIDLKFFFVRAGMMGWLLIN
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HIPPFFSIOGGWLLHNKVELTVPALVVNCLVPLIGYMVFRGANKQKHIFKXNPKTPI
WGKPPVVVGGKLLVSGYWGIARHCNYLGDLMLALSFSLPCGISSPVPYFYPIYLILL
IWRRRRDSVRCAEXYKEIWARYLRLVPWRILPPVY"
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                                       Jobses 1 to 2828)
Jang,J.C. and Sheen,J.
Direct Submission
Submitted (03-MAY-2000) Horticulture and Crop Science, The Ohio State University, 310A Kottman Hall, 2021 Coffey Rd, Columbus, OH 43210, USA
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/organ.sm="Arabidopsis thaliana"
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LYVJGRSSSNKGSSLKPHVSGNLVHDWWFGIQLNPQFMSIDLKFFFVRAGMMGWLLIN
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LHIPFFSIQGWLLHNKCHYQIFCALVILDYFNHEEYMTSTWDIJAERJGFMLVFGDL
WGKPPVVVGGKLLVSGYWGIARHCYVLGDLMLALSFSLPCGISSPVPYFYPITLL
WRERRDEVRCAEKYKEIWAEYLLVPWRILDFVY"
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/translation="MSMHFRNKAWIILAILCFSSLIHSTEAVVTYDHKALIINGQRRI
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                                                                                                       ATF8J2 100-AUG-2000 ATF8J2 PLN 02-AUG-2000 ATBJG0psis thaliana DNA chromosome 3, BAC clone F8J2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: Chackedming.ide, mayeredmips.biochem.mgg.de, mayeredmips.biochem.mgg.de, mayeredmips.biochem.mgg.de, ropered coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue deaston Cremieux, BP191, 91006 Evry Cedex, France; http://www.genoscope.cns.fr on Apr 20, 2000 this sequence version replaced gi:6434218.

Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
                                                                                                                                                                                                                                                                                                                                                                                             Nyakatura, G., Farrmann, B., Dauner, D., Sterr, W., Holland, R., Weichselgartner, M., Mewes, H. W., Rudd, S., Lemcke, K., Mayer, K.F.X., Ouetier, F. and Salanoubat, M.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EU Arabidopsis sequencing, project.
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DEFINITION
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JOURNAL
                                                  RESULT 13
ATF8J2/c
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intr	.,	THE	exon	inti	exou	intr	i co		intron	exon	i		exon	gene	gene	CDS			ехоп	intron	exon	Alignment	Score: Percent S	Best Local Query Match DB:	US-10-069-427-6	ò	op 20
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25 y	Qy 60 uAlaSerGyTyrTrp		DD 54148 TIACCTIGGCGACTIGAIGCTIGCTCTCACTTGCCATGTGGAATAAGGTAACT 54089 QY 89	QY 89 80<	53968 AGTCTAAAGCTTTCAAGTTCATTTCCCAAAGCTGTTTTTATGATATTTTGTCTTGTGTAT 5390 90SerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuAr 108	Db 53908 TCTCAGTTCTCCGGTTCCATATTTCTACCCGATATACCTTCTGATACTATTGATATGAGG 53849 Oy 108 GGluargargaspGlualaargCysSerGlnLysTyrargGlulleTrpAlaGluTyrCy 128	Qy 128 sLysLeuValProTrpArgIleLeuProTyrValTyr 140 :::	RESULT 14 AR427913 LOCUS LOCUS DEFINITION Sequence 10 from patent US 6639130. VERSION AR427913 VERSION AR427913.1 GI:40186948 KEYWORDS VERSION ARATORIAN ARA	Unclassif 1 (bases Jang, JC Plant ste Patent: U	Source (1.27) /organism="unknown" /mol_type="genomic DNA" Alignment Scores:

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                      REFERENCE (bases 1 to 6587)
AUTHORS Jang, J.-C. and Sheen, J.
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Search completed: June 14, 2004, 12:18:11 Job time : 2253.35 secs

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Sequence 4, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 11, Appl
Sequence 3702, Ap
Sequence 864, Appl
Sequence 54, Appli
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Sequence 4, Appli
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Sequence 24, Appli
Sequence 21541, A
Sequence 21541, A
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84.5%; Score 638; DB 4; Length 14.
Best Local Similarity 82.4%; Pred. No. 2.4e-69;
Matches 112; Conservative 13; Mismatches 11; Indels
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Patent No. 6639130
GENERAL INFORMATION:
APPLICANT: Jang, Jyan-Chyun
APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES:
FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT APLICATION NUMBER: 06/022,086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-09-342-653-4
; Sequence 4, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins;
; CURRENT PAPLICATION NUMBER: US/09/342,653
; CURRENT PELING DATE: 1999-06-29
; EARLIER RILING DATE: 1999-06-29
; EARLIER PILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
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US-09-255-91A-26052
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US-09-618-125-9
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; ORGANISM: Oryza sativa
US-09-342-653-4
  RESULT 2
US-08-879-337-1
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Sequence 1, Appli
Sequence 6, Appli
                                                                                                                                                         June 14, 2004, 14:36:55 ; Search time 9.35167 Seconds (without alignments) 772.871 Million cell updates/sec
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Sequence 2, Ay
Sequence 31, Ay
Sequence 6, Ay
Sequence 5, Ay
Sequence 2040
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-879-337-1

US-09-342-653-7

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US-08-931-047-2

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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - protein search, using sw model
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Perfect score:
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Maximum DB seq
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NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
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                                                                     LENGTH: 418
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                                                                                                                                                                                                                                                                                                                                                                                                             295 GIARRCNYLGDLMLALSFSLPCGISSPVPYFYPIYLLILLIWRERRDEVRCAEKYKEIWA 354
                                                                                                                                                                                                                                                                                                                     235 NKVELIVPALVVNCLVFLIGYMVFRGANKQKHIFKKNPKTPIWGKPPVVVGGKLLVSGYW 294
                                                                                                                                                                                                                                                                                                                                                                                      66 GIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSOKYREIWA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LASGYWGIARHCNYLGDLLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQK 119
                                                                                                                                                                                                                                                                                           6 NKVELSLISGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVVGGKLLASGYW 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 LVSGYWGIARHCNYLGDLLLALSFSLPCGASSVIPYFYTYLLILLIWRERRDEARCSEK 60
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                                                                                                                                                                                                   Query Match 79.7%; Score 602; DB 4; Length 368; Best Local Similarity 79.1%; Pred. No. 1.7e-64; Matches 106; Conservative 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 55.5%; Score 419; DB 4; Length 81; Best Local Similarity 90.1%; Pred. No. 3.4e-43; Matches 73; Conservative 5; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cahoon, Rebecca E.
APPLICANT: Cahoon, Rebecca E.
TITLE OF INVENTION: Chromatin Associated Froteins
TITLE OF INVENTION: Chromatin Associated Froteins
FILE REPERENCE: BB-1118
CURRENT APPLICATION NUMBER: US/09/342,653
CURRENT FILING DATE: 1999-06-29
EARLIER FILING DATE: 1999-06-29
SEARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 7
SOFTWARE Microsoft Office 97
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7. Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REPERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CRRENT FILING DATE: 1999-06-29
; EARLIER FILING DATE: JULY 14, 1998
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 YREIWAEYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YKDIWAEYCKLVPWRILPYVY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09342653; Patent No. 6306632; GENERAL INFORMATION:
                                                                                                                ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-879-337-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 EYCKLVPWRILPYV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      355 EYLRLVPWRILPYV 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Triticum aestivum
US-09-342-653-6
                                                                                          LENGTH: 368
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US-09-342-653-6
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                                                                  SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                 75 GDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIWAEYCKLVPWR 134
                                                                                                                                                                                          19 LCIF-LIGYLVFRGANKQKHVFKKDPKAP-IWGKP--PKVVGGKLLASGYWGIARHCNYL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GDLLIALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIWAEYCKLVPWR
                                                                                                                                                4; Gaps
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| Sequence 9, Application US/08879337B
| Sequence 9, Application US/08879337B
| Patent No. 6339130
| GENERAL INFORMATION:
| APPLICANT: Jang, Jyan-Chyun
| APPLICANT: Sheen, Jen
| TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
| PILE REPERRICE: 00786/338001
| CURRENT APPLICATION UNMBER: US/08/879,337B
| CURRENT FILING DATE: 1997-06-20
| SARLIER APPLICATION NUMBER: 60/022,086
| SARLIER PILING DATE: 1996-06-21
| NUMBER OF SEQ ID NOS: 24
                                                                                            48.5%; Score 366; DB 4; Length 418; 54.8%; Pred. No. 6.8e-36; tive 20; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.0%; Pred. No. 1.5e-35;
Matches 66; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Chromatin Associated Proteins
FILE REFERENCE: BB-1118
CURRENT APPLICATION NUMBER: US/09/342,653
CURRENT FILING DATE: 1999-06-29
EARLIER PILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-342-653-2
Sequence 2, Application US/09342653
; Patent No. 6306632
                                                                                              Query Match
Best Local Similarity 54.8%
Matches 69; Conservative
TYPE: PRT
GRGANISM: Homo sapiens
US-09-342-653-7
                                                                                                                                                                                                                                                                                                                                                                                                                                            413 IMPYIY 418
                                                                                                                                                                                                                                                                                                                                                                                                  135 ILPYVY 140
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US-09-342-653-2
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UMBER OF SEQUENCES:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 WWGMARHINYEGDWIMAWAWCIDPAGFGSPIPYFYVAYFGVLLVHRNARDDHKCRVKXGED 407
                                                                                                                                                                                                                                                                                                                                    65 WGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIW 124
                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                               16 LANLCIF--LIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVV------GGKLLASGY
                                                                                                                                                                                                                                                                         8 VELSILISGLANLCIFLIGYLVFRGANKQKHVFKXDPKAPIWGKPPKVV----GGKLLASG
                                                                                                                                                        Query Match
Best Local Similarity 48.5%; Pred. No. 1.9e-33;
Matches 66; Conservative 22; Mismatches 31; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Gaps
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; Sequence 5, Application US/08879337B
; Patent No. 6639130
; Patent No. 6639130
; Patent No. 6639130
; APPILCANT: Jang, Jyan-Chyun
; APPILCANT: Sheen, Jen
; TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
; FILE REFERENCE: 00708/338001
; CURRENT APPLICATION NUMBER: US/08/879,337B
; CURRENT FILING DATE: 1995-06-20
; EARLIER APPLICATION NUMBER: 60/022,086
; EARLIER PILING DATE: 1996-06-21
; NUMBER OF SEQ ID NOS: 24
; SOFTHARE: PASELED for Windows Version 4.0
; SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.2%; Score 341.5; DB 4; Length 424; 48.9%; Pred. No. 6.4e-33; tive 22; Mismatches 43; Indels 5
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APPLICANT: Bard, Martin
APPLICANT: Kirsch, Donald R.
TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
Patent No. 5512472
TITLE OF INVENTION: Reductase
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9 LENGTH: 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-08-879-337-5
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; Sequence 3, Application US/08439131A
Patent No. 5512472
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 WAEYCKLVPWRILPYVY 140
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WEKYCKAVKYRIIPYVY 424
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600 EKYCQRVPYRIFPYIY 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
                                                                 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-879-337-9
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Best Local Similarity
Matches 67; Conserva
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24 IGYLVFRGANKOKHVFKK---DPKAPIWGKPPKVVGGKLLASGYWGIARHCNYLGDLLLA 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide PUBLICATION INFORMATION: AUTHORS: Worman, H. J. AUTHORS: Worman, H. J. AUTHORS: Bvans, C. D. AUTHORS: Brans, C. D. AUTHORS: Brans, C. D. TITLE: The Lamin B Receptor of the Nuclear Envelope TITLE: Inner Membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: FROM 190 TO 608
                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SUSTIVARE: Patentin Release #1.0, Version #1.25
SUSTIVARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/439,131A
FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REGISTRATION NUMBER: 30,637
REFRENCE/DOCKET NUMBER: 854-012 (32,141)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5525496
GENERAL INFORMATION:
APPLICANT: MARGAREH H. Lai
APPLICANT: MARGAREH H. Lai
TITLE OF INVENTION: A DNA Sequence Encoding Sterol
Patent No. 5525496
TITLE OF INVENTION: 14
TITLE OF INVENTION: Reductase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 39.8%; Score 300.5; DB 1; Local Similarity 48.7%; Pred. No. 5.7e-28; les 55; Conservative 18; Mismatches 37;
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                        Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL: J. Cell Biol
VOLUME: 111
PAGES: 1535-1542
CORRESPONDENCE ADDRESS:
ADDRESSEE: American C
STREET: One Cyanamid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                               CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                     ZIP: 07470
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US-08-440-674-2
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EARLIER APPLICATION NUMBER: 60/022,086
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                             TYPE: PRT; ORGANISM: Gallus domesticus
US-08-879-337-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                438 amino acids
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.7%
Matches 55; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acidi
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Wayne
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07470
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                                                                                                                         LENGTH: 637
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     360 LAWSLPCGFNHILDYFYVIYFICLLVHREARDEHHCKKKYGLAWSRYCQRVPY 412
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08879337B
Patent No. 6639130
GENERAL INFORMATION:
APPLICANT: Jang, Jyan-Chyun
PAPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILLE REPRENCE: 00786/33801
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT FILING DATE: 1997-06-20
                                                                                                        CAMPUTER TRADABLE FORM:

MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: 1BM PC
COMPUTER: BM PC
COMPUTER: BM PC
COMPUTER: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: May 15, 1995
CLEASSIFICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: May 16, 1993
ATTORNEY/AGENT INFORMATION:
FILING DATE: AUGUSE 16, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan M. Gordon
REGISTRATION NUMBER: 854-P0012 Div (32,141)
TELEPHONE: 201-831-3305
INFORMATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 residues
TTELETH AND GOLD
TYPE: mainto acid
TTELETH AND GOLD
TYPE: mainto acid
TTELETH AND GOLD
TYPE: mainto acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE: (excerpt): The Lamin B Receptor of the TITLE: Nuclear Envelope Inner Membrane JOURNAL: 11 Biology VOLUME: 111 PAGES: 1535-1542 PAGES: Sequence set out in Figure 5, page 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; RELEVANT RESIDUES IN SEQ ID NO: 190 to 608 US-08-440-674-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: nuclear lamin B receptor PUBLICATION INFORMATION: AUTHORS: H.J. Worman, C.D. Evans, and G. AUTHORS: Blobel
: One Cyanamid Plaza Wayne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESCRIPTION: polypeptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                   New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: STRANDEDNESS: SIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Patent No. 5525496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                 07470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-879-337-8
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                                                        Gaps
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                                                                                                                                                                                                                  81 LSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIWAEYCKLVPW 133
                                                                                                                                                                                                                                                  Indels 13;
  DB 4; Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08439131A
Fatent No. 5512472
GENERAL INFORMATION:
APPLICANT: Eat, Martin
APPLICANT: Artin
APPLICANT: Artin
APPLICANT: Artin
APPLICANT: Artin
APPLICANT: Risch, Donald R.
TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
TITLE OF INVENTION: Reductase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSES: Antican Company
STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 438;
39.8%; Score 300.5; DB 4; Length 48.7%; Pred. No. 9.6e-28; tive 18; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER PRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/439,131A
FILING DATE: 11-MAY-1995
CLASSFEICATION: DATA:
APPLICATION NUBER: US 08/107,347
FILING DATE: 16-MG-1993
ATTORNEY/AGENT INFORMATION:
NAME: GO-COO, ALANG-1993
ATTORNEY/AGENT INFORMATION:
NAME: GO-COO, ALANG-1993
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 30,637
TELEPHONE: 201-831-3244
TELEPHONE: 201-831-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.4%; Score 252.5; DB 1; Best Local Similarity 38.1%; Pred. No. 3.8e-22; Matches 53; Conservative 25; Mismatches 48;
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360 DGWAXSQHINYFGDWLISLSWCLATWFQTPLTYYYSLYFATLLLHRQQRDEHKCRLKYG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 SGYWGIARHCNYLGDLILLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 DGWWAKSQHINYFGDWLISLSWCLATWFQTPLTYYYSLYFATLLLHRQQRDEHKCRLKYG 419
  ---GKLENLKSIQTKRGTKLLC 359
                                              62 SGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSOKYR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
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APPLICANT: Sheen, Jen
APPLICANT: Sheen, Jen
APPLICANT: Sheen, Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REFERENCE: 00786/138001
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT APPLICATION NUMBER: US/08/679,337B
ARLIER PILING DATE: 1997-06-20
ARLIER PILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SEQ ID NO 4
LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.4%; Score 252.5; DB 4; Length 438; Best Local Similarity 38.1%; Pred. No. 3.8e-22; Matches 53; Conservative 25; Mismatches 48; Indels 13
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APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE ON TINUENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-20
307 VELGWVKVVGILAIMFLGFHIFHSANKQKSEFRQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
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US-09-49-101A-22
US-09-49-041A-22
; Sequence 22, Application US/09443041A
; Patent No. 6465717
; GENERAL INPORMATION:
; APPLICANT: Famodu, Omolayo O.
                                                                                                                                                                                                                                                                                                   ; Sequence 4, Application US/08879337B; Patent No. 6639130; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                  420 ENWEEYERKVPYKIIPYVY 438
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420 ENWEEYERKVPYKIIPYVY 438
                                                                                                                                          122 EIWAEYCKLVPWRILPYVY 140
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SOFTWARE: Microsoft Office 97
SEQ ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-443-041A-22
                                                                                                                                                                                                                                                         RESULT 13
US-08-879-337-4
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                             62 SGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLUVLRERRDEARCSQXYR 121
    8 VELSLLSGLANLCIFLIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVV-----GGKLLA 61
                                                                                                                        360 DGWWAKSOHINYFGDWLISLSWCLATWFOTPLTYYYSLYFATLLHROORDEHKCRLKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
33.4%; Score 252.5; DB 1; Length 438;
Best Local Similarity 38.1%; Pred. No. 3.8e-22;
Matches 53; Conservative 25; Mismatches 48; Indels 13
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                                                                                                                                                                                                                                                                                                                      US-08-440-674-5.
Sequence 5, Application US/08440674;
Patent No. 5525496;
GENERAL INFORMATION:
APPLICANT: Margaret H. Lai
TITLE OF INVENTION: A DNA Sequence Encoding Sterol
Patent No. 5525496;
TITLE OF INVENTION: 14
TITLE OF INVENTION: Reductase
UNUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   854-P0012 Div (32,141)
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MOLECULE TYPE:
DESCRIPTION: polypeptide
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: Saccharomyces cerevisiae
IMMEDIATE SOURCE: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
FILING DATE: May 15, 1995
CLASSIFICATION: 536
PRIOR APPLICATION: 536
PRIOR PAPLICATION: DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: AUGUST 16, 1993
ATTORNEY, AGENT INPORMATION:
NAVE: ALAN M. GORGON
REGISTRATION NUMBER: 30637
REPREMENCE/POCKET NUMBER: 30637
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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reductase gene
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                                                                                                                                                                                                                 LENGTH: 438 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: New Jersey COUNTRY: USA
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296 ILAGI--LCIY-INY----DCDRQRQEPRRTNGKCSINGKAPSKIVASYQTTNGETKSSL 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LLSGLANLCIFLIGYLVFRGANKQKHVFKK-DPKAPIWGK-PPKVVG------GK 58
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                      20; Gaps
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Best Local Similarity 37.3%; Pred. No. 7.9e-22;
Matches 53; Conservative 31; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LLSGLANLCIFLIGYLVFRGANKQKHVFKK-DPKAPIWGK-PPKVV--
                                                                                                                                                                                                                                                                                        RESULT 15
US-09-443-041A-18
Sequence 18, Application US/09443041A
Federate No. 6465717
GENERAL INFORMATION:
APPLICANT: Femodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
FILE OF INVENTION: Sterol Metabolism Enzymes
FILE OF INVENTION: Sterol Metabolism Enzymes
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT APPLICATION NUMBER: 60/109,283
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1999-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
LENGTH: 430
TWOST INCOME.
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Job time : 10.3517 secs
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ORGANISM: Oryza sativa
US-09-443-041A-18
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June 14, 2004, 14:31:29; Search time 28.6051 Seconds (without alignments) 1382.853 Million cell updates/sec
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755
1 PRVRXNKVELSLLSGLANLC.....REIWAEYCKLVPWRILPYVY 140
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                    1586107 seqs, 282547505 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
2: geneseqp2000s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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seq length: 200000000
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Maximum DB
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                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Abj25553 Aspergill	Aar71934 Sterol-de	Aaw01975 Saccharom	Aar98333 Saccharom				66	298	597	539	38	337	Abp53721 Arabidops	Abp53717 Arabidops	Aaw03567 Arabidops	Add69617 Human REM		Abb66565 Drosophil	Abb62216 Drosophil
ABJ25553	AAR71934	AAW01975	AAR98333	ABG73987	ABG73985	ABG73986	AAG23599	AAG23598	AAG23597	AAG53539	AAG53538	AAG53537	ABP53721	ABP53717	AAW03567	ADD69617	ADE07998	ABB66565	ABB62216
'n					430 6						118 3						350 7	716 4	131 4
2.5 34.8	52.5 33.4	2.5 33.4	52.5 33.4	50 33.1	47 32.7	5 32.3	25 29.8	25 29.8	25 29.8	29.8	25 29.8	25 29.8	25 29.8	25 29.8	11 27.9	6.5 27.4	76.5 23.4	9 21.1	24 16.4
56	27	28	29	30		32	33	34	35	36	37	38	39	40	41	42	43	44	

ALIGNMENTS

The present sequence is that of a soybean sterol delta-14 reductase polypeptide, as deduced from a partial coding sequence from the full insert sequence of a clone (see AAF30676) isolated from a cyst nematode-infected soybean 8-day-old theory in the predicted polypeptide shows amino acid sequence homology to Arabidopsis thaliana and Ascobolus immersus sterol delta-14 reductases. The invention relates to sterol delta-14 reductases. It also relates to transgenic plants comprising the polymucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the sterol delta-14 reductase, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the catantiformed host cell. The availability of plant sterol delta-14 reductase genes will provide a means of altering sterol production Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase. Soybean, sterol delta-14 reductase; transgenic plant; herbicide; fungicide. Soybean sterol delta-14 reductase polypeptide. & COEI. Claim 1(b); Page 38; 45pp; English. AAB20380 standard; protein; 140 AA. 99US-0156820P. 27-SEP-2000; 2000WO-US026442. (DUPO) DU PONT DE NEMOURS (first entry) Famodu OO, Kinney AJ; WPI; 2001-266146/27. N-PSDB; AAF30676. WO200123539-A2. 30-SEP-1999; 05-APR-2001. 11-JUN-2001 Glycine max. AAB20380;

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and/or composition of plants, to identify compounds that may be useful as novel herbicides and fungicides, and to identify mutants of these genes that are resistant to these herbicides and will enable the production of
                                                                                                                                                                                                                                                                          61 ASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSOKY 120
                                                                                                                                                                                                                                                                                             61 ASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQXY 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel gene encoding sterol delta-14 reductase useful for transgenic plant
production with altered sterol delta-14 reductase.
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                                                                                                                                                                                                   1 PRVRKNKVELSLLSGLANLCIFLIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVVGGKLL
                                                                                                                                                                                                                          PRVRKNKVELSLLSGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVVGGKLL
                                                                                                                                                                 Gaps
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fungicide.
                                                                                                                                                                  ö
                                                                                                                            Length 140;
                                                                                                                                                               0; Indels
                                                                                                                            100.0%; Score 755; DB 4;
100.0%; Pred. No. 5.5e-84;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1(b); Page 36-38; 45pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB20379 standard; protein; 374 AA.
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                                                                                                                                                                                                                                                                                                                                                 REIWAEYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                                                      (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corn sterol delta-14 reductase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0156820P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                       herbicide-resistant crops
                                                                                                                                                                 Matches 140; Conservative
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                                                                                                                          Query Match
Best Local Similarity
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                                                                                            Sequence 140 AA;
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The present sequence is that of soybean sterol delta-14 reductase, as deduced from a full-length coding sequence from the full insert sequence of a clone (see AAF30677) isolated from a soybean shoot meristem cDNA library. The predicted protein shows amino acid sequence homology to Arabidopsis thaliana and Ascobolus immereus sterol delta-14 reductases. The invention relates to sterol delta-14 reductase polynucleotides and polypeptides and to transgenic plants comprising the polynucleotides and polypeptides and to transgenic plants comprising the polynucleotides and polypeptides and to transgenic plants comprising the polynucleotides and polypeptides and the construction of a chimeric gene results in production of the sterol delta-14 reductase, in sense or antisense orientation, where expression of the chimeric gene results in production of a valiability of plant sterol delta-14 reductase genes will provide a means of altering sterol production and/or composition of plants, to identify compounds that may be useful as novel herbicides and fungicides, and to identify mutants of these genes that are resistant to these therbicides and will enable the production of herbicide-resistant crops
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                                                                                                                                                                                            240 NSVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPINGKPFKVIGGKLLASGYM 299
                                                                                                                                                                                                                                               66 GIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIWA 125
                                                                                                                                                                                                                                                                   Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase.
that are resistant to these herbicides and will enable the production of herbicide-resistant crops
                                                                                                                                                                         6 NKVELSLLSGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVVGGKLLASGYW
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soybean; sterol delta-14 reductase; transgenic plant; herbicide;
                                                                                                                                     ö
                                                                                              Length 374;
                                                                                                                                     10; Indels
                                                                                                83.0%; Score 627; DB 4;
83.0%; Pred. No. 9.4e-68;
iive 13; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB20381 standard; protein; 369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soybean sterol delta-14 reductase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2000; 2000WO-US026442.
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                                                                                                                                                                                                                                                                                                                          126 EYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                              360 EYRKLVPWRILPYVY
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N-PSDB; AAF30677.
                                                                                                                  Similarity
                                                            Sequence 374 AA;
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                                                                                                                    Best Local Sim.
Matches 112;
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                                                                                                  Query Match
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9905-0141287P.
9905-0141842P.
9905-0142952P.
9905-0142920P.
9905-0142920P.
9905-0142920P.
9905-0142924P.
9905-0144005F.
9905-0144332P.
9905-0144334P.
9905-014508P.
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               9905-0136021P-
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9905-0137222P-
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9905-0138640P-
9905-0139452P-
9905-0139462P-
9905-0139462P-
9905-0139462P-
9905-0139462P-
294
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                                                                                                                                                                       6 NKVELSLLSGLANLCIFLIGYLVFRGANKOKHVFKKDPKAPIWGKPPKVVGGKLLASGYW
                                                                                                       ;
0
                                                           82.3%; Score 621; DB 4; Length 369;
82.2%; Pred. No. 5e-67;
ive 13; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 18066.
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99US-0123180P

99US-0126264P

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99US-0126244P

99US-0127464P

99US-0128234P

99US-0130810P

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99US-0131848P

99US-0132484P

99US-013421P

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99US-0134218P
                                                                                                                                                                                                                                                                                                             EYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 82.2%
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000 (first entry)
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                        Sequence 369 AA;
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09-WAR-1999

25-WAR-1999

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PR (4-AMG-1999) 99US-0147308P.
PR (5-AMG-1999) 99US-0147308P.
PR (5-AMG-1999) 99US-0147308P.
PR (5-AMG-1999) 99US-0147308P.
PR (5-AMG-1999) 99US-0147308P.
PR (10-AMG-1999) 99US-0147308P.
PR (10-AMG-1999) 99US-0147318P.
PR (10-AMG-1999) 99US-0147318P.
PR (10-AMG-1999) 99US-0149318P.
PR (10-AMG-1999) 99US-0149328P.
PR (10-AMG-1999) 99US-0151339P.
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                                                                                            96 NKVELTIPAIUVNCLVFLIGYMVFRGANKQKHIFKKNPKTPIWGKPPVVVGGKLLVSGYW 155
                                                                                                                        66 GIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSOKYREIWA 125
                                                                                                                                   156 GIARHCNYLGDLMLALSFSLPCGISSPVPYFYPIXLLILLINFERRDEVRCAEKYKEIWA 215
                                                                                 65
                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                6 NKVELSLISGLANLCIFLIGYLVFRGANKQKHVFKKDPKAPINGKPPKVVGGKLLASGYW
                                                             Gaps
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                                         DB 3; Length 230;
                                                            13; Indels
                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 18065.
                                        Query Match
80.8%; Score 610; DB 3.
Best Local Similarity 79.3%; Pred. No. 6e-66;
Matches 107; Conservative 15; Mismatches
                                                                                                                                                                                                                                    AAG17152 standard; protein; 365 AA.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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99US-012348P.
99US-0125784P.
99US-0125784P.
99US-0126264P.
99US-0127462P.
99US-0128234P.
99US-0128234P.
99US-0130891P.
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99US-0132487P.
                                                                                                                                                                EYCKLVPWRILPYVY 140
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                                                                                                                                                                                                                                                                            (first entry)
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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09-WAR-1999;
23-MAR-1999;
25-MAR-1999;
06-APR-1999;
06-APR-1999;
16-APR-1999;
19-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
06-MAY-1999;
06-MAY-1999;
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11-MAY-1999;
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01-JUN-1999;
03-JUN-1999;
04-JUN-1999;
07-JUN-1999;
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                                          80.8%; Score 610; DB 3; 79.3%; Pred. No. 1.1e-65; ive 15; Mismatches 13;
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Best Local Similarity 79.3
Matches 107; Conservative
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28-OCT-1999;
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GIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIWA 125
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                                                                                                       NKVELSLLSGLANLCIFLIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVVGGKLLASGYW
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80.8%; Score 610; DB 3;
Best Local Similarity 79.3%; Pred. No. 1.1e-65;
Matches 107; Conservative 15; Mismatches 13.
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EYLRLVPWRILPYVY 369
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80.7%; Score 609; DB 3;
Best Local Similarity 79.3%; Pred. No. 7.9e-66;
Matches 107; Conservative 15; Mismatches 13
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                                                                                                                   Query Match 80.7%; Score 609; DB 3; Length 365; Best Local Similarity 79.3%; Pred. No. 1.5e-65; Matches 107; Conservative 15; Mismatches 13; Indels
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351 EYLRLVPWRILPYVY 365
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N-PSDB; AAV04237, AAV04238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana.
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26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
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Reduced production of C14SR can increase the life-span of plants and produce plants having reduced and more compact proportions.

Overproduction is useful for enhancing the production of medically or agriculturally useful steroid compounds. C14SR polypeptides are also useful for the development of enzyme inhibitors of the steroi
                                                                                                                                                                   Gaps
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Best Local Similarity (1973%) Pred. No. 1.5e-65;
Matches 107; Conservative (15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 47791
                                                                                                                                                                                                                                                                                                                                                                                                       AAG38706 standard; protein; 369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-01218025P.
99US-0123180P.
99US-0125788P.
99US-0126264P.
99US-0126264P.
99US-012624P.
99US-012624P.
99US-0130414P.
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99US-0130449P.
99US-0131048P.
99US-0132488P.
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                                                                                                                                                                                                                                                                                                         EYCKLVPWRILPYVY 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana
                                                                                                             Sequence 369 AA;
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03-MAR-1999
25-MAR-1999
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06-OCT-1999;
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16-AUG-1999;
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27-AUG-1999;
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                                                                                                                                                                                                                                                                                               295 GIARHCNYLGDLMLALSFSLPCGISSPVPYFYPIYLLILLIHWERRDEVRCAEKYKEIWA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of human genes or expression products in an endometrial sample suspected of being cancerous. The human genes of the invention are differentially expressed in breast tumours characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products.
                                                                                                                                                                                                                                    235 NKVELTVPAIVVNCLVFLIGYMVFRGANKQKHIFKKNPKTPIMGKPPVVVGGKLLVSGYM 294
                                                                                                                                                                                                                                                                               66 GIARHCHYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSOKYREIWA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing breast cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant tissue.
                                                                                                                                                                                                                      65
                                                                                                                                                                                                                    6 NKVELSLLSGLANLCIFLIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVVGGKLLASGYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; diagnosis of breast cancer; endometrial cancer; breast tumour; MAI; mitotic activity index; cytostatic.
                                                                                                                                                                                       Gaps
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                                                                                                                                                      80.7%; Score 609; DB 3; Length 369; 79.3%; Pred. No. 1.5e-65; ive 15; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 37; Page 183-185; 219pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
(BAAK/) BAAK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU84347 standard; protein; 615 AA
99US-0161406P.
99US-0161359P.
99US-0161359P.
99US-0161360P.
99US-0161920P.
99US-0161920P.
99US-0161932P.
                                                                                                                                                                                                                                                                                                                                        126 EYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                                          355 EYLRLVPWRILPYVY 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-2001; 2001WO-US023642
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                     al Similarity 79.3
107, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-180084/23.
N-PSDB; ABK35567.
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 25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
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                                                                                                                                                        Query Match
                                                                                                                                                                                     Matches
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The present invention relates to 26 secreted human proteins. The proteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperpioliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and any involving abnormal angiogenesis, neurodegeneration
                                                                                                                                              195 HASKLLVSGFWGVARHFNYVGDLMGSLAYCLACGGGHLLPYFYIIYMAILLTHRCLRDEH 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56 -GGKLLASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLULRERRDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's and diabetic retinopathy.
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                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 VELSLLSGLANLCIFLIGYLVFRGANKOKHVFKK-DPKAPIWGKPPKVV----
                                                                  VELSLLSGLANLCIFLIGYLVFRGANKQKHVFKK-DPKAPIWGKPPKVV----
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      Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein, gene therapy; vaccine; cancer; leukemia, autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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      DB 4;
                      . Be-30;
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    Score 319.5; D
Pred. No. 2.8e-
16; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 514-515; 525pp; English
                                                                                                                                                                                        RCSOKYREIWAEYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GA;
                                                                                                                                                                                                          255 RCASKYGRDWERYTAAVPYRLLPGIF
                                                                                                                                                                                                                                                                                                  AAB60760 standard; peptide; 280 AA
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42.3%; Scor
43.2%; Preć
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                                                                                                                                                                                                                                                                                                                                                                                            Gene 13 related peptide #2
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       infectious diseases
                                   63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071148/08.
                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JUN-11999;
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Best Local Simi
Matches 63;
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        Query Match
Best Local S:
Matches 63,
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                                                                                                                                                                                                                                                                     RESULT 13
AAB60760
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                                                                                                                                                                                                                       539
                                                                                                                                                                                                                                                                                    599
                                                                                                                                                                                                                                                    WGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEARCSQKYREIW 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease
 The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment of endometrial cancer. AAU84311-AAU8436 expressent the human proteins of the invention that are differentially expressed in breast cancer tissue
                                                                                                                                                                                                            540 WGFVRHDNYLGDLIMALAWSLPCGFNHILPYFYIIYFTMLLVHRBARDEYHCKKKKGVAW
                                                                                                                                                                                          ---GGKLLASGY
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's and diabetic retinopathy.
                                                                                                                             DB 5; Length 615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection.
                                                                                                                                                                                          16 LANLCIF--LIGYLVFRGANKQKHVFKKDPKAPIWGKPPKVV-----
                                                                                                                                                            Indels
                                                                                                                                                            31;
                                                                                                                            46.0%; Score 347.5; DB 48.5%; Pred. No. 3e-33; iive 22; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAB60759 standard, peptide, 280
                                                                                                                                                                                                                                                                                                                 125 AEYCKLVPWRILPYVY 140
                                                                                                                                                                                                                                                                                                                                 EKYCQRVPYRIFPYIY 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 13 related peptide #1
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                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-071148/08.
                                                                                                                                            Similarity
                                                                                                Sequence 615 AA;
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                                                                                                                             Query Match
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This invention describes a human Delta7-sterol reductase. The encoding DNA can be used to diagnose or correct human Delta7-sterol reductase gene defects e.g. hereditary Smith-Lemil-Opitz syndrome, and to produce the recombinant Delta7-sterol reductase polypeptide, which can be used to replace a defective Delta7-sterol reductase enzyme in humans or other animals. It is also useful to screen for Delta7-sterol reductase inhibitors or to introduce and remove double bonds in synthetic and naturally occurring organic polymeric ring systems (Delta 7-sterol reductase catalyses the conversion of 7-dehydrocholesterol to
                     390 HHSKLLVSGFWGVARHFNYVGDLMGSLAYCLACGGGHLLPYFYIIYYAILLTHRCLRDEH 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GGKILASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Delta7-sterol reductase polypeptide - useful for diagnosis or
treatment of genetic defects e.g. hereditary Smith-Lemli-Opitz syndrome.
                                                                                                                                                                                                                                                                                                              Human; Delta7-sterol reductase; hereditary; Smith-Lemli-Opitz syndrome; diagnosis; screening; double bond removal; 7-dehydrocholesterol; organic polymeric ring; cholesterol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 -GGKLLASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLULRERRDEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VELSLISGLANLCIFLIGYLVFRGANKOKHVFKK-DPKAPIWGKPPKVV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.3%; Score 319.5; DB 2; Length 475; 43.2%; Pred. No. 5.7e-30; ive 26; Mismatches 44; Indels 13
                                                                  115 RCSOKYREIWAEYCKLVPWRILPYVY 140
                                                                                    450 RCASKYGRDWERYTAAVPYRLLPGIF 475
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                                                                                                                                                                                                                                                                                  Human Delta7-sterol reductase protein
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                                                                                                                                                                                  AAW93573 standard; protein; 475 AA
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N-PSDB; AAX23387.
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63; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human secreted protein. Human secreted protein polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include mutritional activity, cytokine and call proliferation/differentiation activity, hammes stimulating (e.g. as vaccines) or suppressing activity, hammestopoises regulating activity, tissue growth activity, activity, chemotactic/chemokinetic activity, receptor/ligand activity, and hammatory activity, cadherin/tumour invasion suppressor activity, and tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
 -GGKLLASGYWGIARHCNYLGDLLLALSFSLPCGVSSVVPYFYPTYLLILLVLRERRDEA 114
                     195 HHSKLLVSGFWGVARHFNYVGDLMGSLAYCLACGGGHLLPYFYIIYMAILLTHRCLRDEH 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, secreted protein; nutrition, cytokine, cell proliferation; differentiation; immune stimulating; vaccine; suppression, gene therapy; haematopoiesis regulation; tissue growth; activin; inhibin; cadherin; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour invasion suppressor; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins-Racie LA, Merberg D;
RJ, Wong GG, Clark HF, Fechtel K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides encoding secreted human proteins derived from, e.g. fetal brain potentially used as immunostimulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VELSLISGLANLCIFLIGYLVFRGANKQKHVFKK-DPKAPIWGKPPKVV------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.3%; Score 319.5; DB 2; Length 475; llarity 43.2%; Pred. No. 5.7e-30; Conservative 26; Mismatches 44; Indels 13
                                                                                                                                                                                                                                                                                  Human secreted protein clone pj323_2 protein sequence.
                                                                    RCSQKYREIWAEYCKLVPWRILPYVY 140
                                                                                       ||: || :: || :: || :: || :: RCASKYGRDWERYTAAVPYRLLPGIF 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccoy JM, Lavallie ER,
Agostino MJ, Steininger
                                                                                                                                                                                    AAY29333 standard; protein; 475 AA.
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99US-00235609.
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Treacy M,
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Aax 90448
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-MODEL=frame+ pan.model.-PEN=xlh
-Q=/Cgn2_1/USPTO_spool/US10069427/runat_14062004_104800_24751/app_query.fasta_1.846
-Q=/Cgn2_1/USPTO_spool/US10069427/runat_14062004_I04800_24751/app_query.fasta_1.846
-Q=/Cgn2_1/USPTO_spool/US10069427/runat_END=-I-MATRIX=blosum62_-I-MODEL=0.
-LOOPEXT=0.UNITS=bits -STRAT=1.END=-1.MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45 -DOCALIGN=200_THR_SCORE_EDCT_THR_ANX=100_THR_INN=0.ALIGN=15
-MODEL=LOCAL.-OUTFMT=pto.-NORM=ext.-HEABSIZE=500_-MINIEN=0.MAXLEN=>00000000
-USFR=US10069427_GCN_1_1 586_Grunat_14062004_104800_24751.NCPU=6_-ICPU=3
-NO MYAP -LARGEQUERY -NGG_SCORES=0.MAIT -DSPELOCK=100_-LONGLOG
-DEV_TIMEOUT=120_-WARN_TIMEOUT=0.5_-PELORED=10_-XGAPBEXT=0.5_-FGAPOP=6
-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELORET=7
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                         nucleic search, using frame_plus_p2n model
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Result No.

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The present sequence is that of the full insert sequence of clone sr23c.pk009.c1, which includes a partial coding region for soybean sterol clata-14 reductase (see AAB2030). The clone was isolated from a cDNA library prepared from soybean 8-day-old root infected with cyst mematode, following database homology searches. The predicted polypeptide shows manerus sterol delta-14 reductases. The predicted polypeptide shows immersus sterol delta-14 reductases. The invention relates to isolated polynucleotides encoding sterol delta-14 reductases and to transgenic plants comprising such polynucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the sterol delta-14 reductase, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell. The availability of plant sterol delta and reductase genes will provide a means of altering sterol production and movel herbicides and fungicides, and to identify compounds that may be useful as novel herbicides and these herbicides and will enable the production of that are resistant to these herbicides and will enable the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArgIleLeuProTyrValTyr 140
                                                                                             Novel gene encoding sterol delta-14 reductase useful for transgenic plant
production with altered sterol delta-14 reductase.
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WPI; 2001-266146/27
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ADD17001 standard; DNA; 625 BP.

ADD17001;

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This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought phenotypes can affect growth regulation i.e. useful for creating dwarf phenotypes can affect growth regulation i.e. useful for creating dwarf ovarieties, exhibit resistance to insects or heat stress, confer changes in pigment content such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises generating transgenic plants, as well as reproducibly altering the visual phenotype of plant seeds, plant tissues and plant cells containing the plants confers an alteriar phenotype when expressed in DNA sequence that confers an altered visual phenotype when expressed in plants, the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 TACTTAGTGTTCAGAGGTGCCAACAAGCAGAAGCATATGTTTAAAAAGAATCCCAAGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProlleTrpGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyrTrp
                                                                   ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistance;
                                 DNA (SeqID 1069) that confers an altered visual phenotype in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid derived from Nicotiana benthamiana, C
sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for
conferring altered visual phenotypes in plants.
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                                                                                                                                                                                                                                                                                                                                                                                                            Ruegger M, Larrinua I, Shukla V;
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                              30-AUG-2002; 2002WO-US027880.
                                                                                                                                                                                                                                                                                                                  31-AUG-2001; 2001US-0316326P.
                                                                                                                                                                                                                                                                                                                                                       DOWC ) DOW CHEM CO. DOWC ) DOW AGROSCIENCES LLC.
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630.00
92.59%
82.22%
83.44%
(first entry)
                                                                                                                                heat stress; transgenic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-300858/29.
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Query Match:
                                                                                                                                                                                                     WO2003020741-A1.
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                                                                                                                                                                 Unidentified
15-JAN-2004
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Sequence 1631 BP; 392 A; 330 C; 353 G; 556 T; 0 U; 0 Other;
                        Alignment Scores:
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                                                                               Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the full-insert sequence of clone p0097.cgrau(57ra;fis, coding for corn sterol delta-14 reductase (see AAB20379). The clone was isolated from a cDNA library prepared from corn by whorl section + ECB1, following database homology searches. The predicted polypeptide shows amino acid sequence homology to Arabidopsis thaliams and Ascobolus immersus sterol delta-14 reductases. The invention relates to isolated polymenties encoding sterol delta-14 reductases and to transgenic plants comprising such polymucleotides. It also relates to transgenic plants comprising such polymucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the sterol delta-14 reductases will provide a means of altered levels of the enzyme in a transformed host cell. The availability of plant control delta-14 reductase genes will provide a means of altering sterol production and/or composition of plants, to identify compounds that may these genes that are resistant to these herbicides and will enable the production of herbicide-resistant crops
                        448
                                             105
                                                                  508
                                                                                        ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
                                                                                                      Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase.
 85
             889 GGCATTGCTCGACACTGTAATTACCTTGGAGATTTGTTGCTGGCATTGTCATTTAGTTTG
                                             CCTTGTGGGGATAAGTTCCGGGGTTCCATATTACCCCCATATATCTTCTTGTT
 GlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu
                                                                                                                                                                                                                                                                                                  Corn; maize; sterol delta-14 reductase; transgenic plant; herbicide;
                                                                                                                                    Corn sterol delta-14 reductase clone p0097.cgrau67ra:fis.
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74. .1198
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P-PSDB; AAB20379.
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                                                                                                                                                                                                                                                                                                             fungicide; ss.
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106 ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
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                                                                                                                                                                                                                                                 46 ProlleTrpGlyLysProProLysValValGlyGlyLyLysLeuLeuAlaSerGlyTyrTrp
                                                                                                                                                                                                                                                                                                               66 GlylleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeu
                                                                                                                                   AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGly
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   1631
112
13
10
0
 Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                         Gaps:
                                                                                                       US-10-069-427-6 (1-140) x AAF30675 (1-1631)
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64. .1173
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7.44e-69
627.00
92.59%
82.96%
83.05%
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                             Percent Similarity:
Best Local Similarity:
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03-JUN-1
     The present sequence is that of the full insert sequence of clone sem.pk0031.d12, which includes a full-length coding region for soybean steroid delta-14 reductaes 6 fee AAB20381). The clone was isolated from a soybean shoot meristem cDNA library, following homology searches. The predicted protein shows amino acid sequence homology to Arabidopsis thalians and Ascobolus immersus steroid delta-14 reductases. The invention relates to isolated polymucleotides encoding steroid delta-14 reductases and to transgenic plants comprising such polymucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the steroid delta-14 reductases, in sense or antisense crientation, where expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell. The availability of plant steroid delta-14 reductase genes will provide a means of altering steroid production and/or composition of plants, to identify compounds that may be production of herbicides and fungicides, and to identify mutants of these genes that are resistant to these herbicides and will enable the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1006 CCATGTGGGATAAGTTCACCAATTCCAACTTCTATCCAATTTATCTTCTTATTCTGTTA 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 ValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
                         Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 ProlleTrpGlyLysProProLysValValGlyGlyLysLeuLeuAlaSerGlyTyrTrp 65
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                                                                                                                                                                                                                                                                                                        Sequence 1364 BP; 346 A; 277 C; 296 G; 445 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                               Claim 7; Page 39; 45pp; English
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621.00
91.85%
82.22%
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Best Local Similarity:
P-PSDB; AAB20381.
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
Arabidopsis thaliana DNA fragment SEQ ID NO: 18063
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9905-0128414P
9905-01300449P
9905-0130040P
9905-0130040P
9905-0131449P
9905-0131449P
9905-0132484P
9905-0132484P
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9905-013421P
9905-013421P
9905-013422P
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99US-0139457P.
99US-0139458P.
99US-0139460P.
99US-0139460P.
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99US-0126785P.
99US-0127462P.
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                                                                                    Arabidopsis thaliana
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05-MAY-1999;
06-MAY-1999;
                                                                                                                                             06-SEP-2000
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                  86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeuIleLeuLeu
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contact close bill includes a coding region for a novel C-14 sterol reductase (see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra long life), that displayed a life span that was at least 3 times greater then wild-type plants, was isolated. The ell mutant was isolated by T-DNA tagging, and used to screen cDNA and genomic libraries from a wild-type plant to identify close DI3 and a 6588 by genomic close (see AAV04238). A pura plant C-14 sterol reductase (C145R) is claimed, as are purified DNA encoding C145R, a vector, a method of producing recombinant C145R using transformed plant cells, a transgenic plant that expresses C145R bNA and a seed or cell from such a plant, and methods for detecting and isolating c cusing an antisense construct. The genetic manipulation of plant sterol composition is useful for improving food quality and oil stability, and for regulating the formation of C145R can increase the life-span of properties. Reduced production of C145R can increase the life-span of plants and produce plants having reduced and more compact proportions. Overproduction is useful for enhancing the production of medically or agriculturally useful steroid compounds. C145R polypeptides are also the production of the sterol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAspProLysAla 45
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                                                                                                                                                                                                                                                                      Sequence 1429 BP; 369 A; 269 C; 305 G; 481 T; 0 U; 5 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GluTyrCysLysLeuValProTrpArglleLeuProTyrValTyr 140
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          Claim 7; Fig 14; 71pp; English.
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We crop improvement; ds. KLL gene; transgenic plant, steroid, crop improvement; ds. KL gene; transgenic plant, steroid, crop improvement; ds. Kay

See Arabidopsis thaliana | Arabidopsis | Arabidopsis
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This genomic DNA includes coding exons for a novel C-14 sterol reductase (see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra long life), that displayed a life span that was at least 3 times greater then wild-type plants, was identified. The ell mutant was isolated by T-DNA tagging, and used to screen genomic and cDNA libraries from a wild-type plant to identify the 6588 bp genomic clone and cDNA clone DNA clone DNA tagging, and used to screen genomic clone and cDNA clone DNA clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated plant C-14 sterol reductase gene - used to develop products for the genetic manipulation of a plant sterol biosynthetic pathway to improve plant characteristics.
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Pred. No.:
Score:
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Length:
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1.95e-51 496.00 44.49\$ 39.34% 65.70%

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                                                                                                                                                                  5541
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                                                                                                                                                                                                                                                                               5602 GGTTTCAGGCTATTGGTATGTTATATTTTATCTTCTTTGTTTTTTGCTTGGTTTCGCCA 5661
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                                                                                                                                                                                                                                                                                                                                      5662 TCTCTGTGTTTGATTGTTCATCATGCTGGGAATAAAGAGTTGAAAGTTCCGCAATGACAC 5721
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                                                                                                                                                        40 slysAspProlysAlaProlleTrpGlyLysProProlysValValGlyGlyLysLeuLe
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                                                                                                                                                                                                                                                                                                                                                                                                                          72 nTyrLeuGlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyVal----
                         AsnLysValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIle-Gl
                                                                                                                                       26 ------TyrLeuValPheArgGlyAlaAsnLysGlnLysHisValPheLy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene LBR differentially expressed in breast cancer tissue
                                                                                                                                                                                                                                                      60 uAlaSerGlyTyrTrp-----------
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US-10-069-427-6 (1-140) x AAV04238 (1-6588)
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The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of human genes or expression products in an endometrial sample suspected of being cancerous. The human genes of characterised as high or low MAI (mitoric activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment of endometrial cancer. ABX35531-ABX35531 represent the human genes of the invention that are differentially expressed in breast cancer tissue
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                                                                                                                                                                                                                                                                                      (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
(BAAK/) BAAK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 94-96; 219pp; English.
                                                                                                                                                                27-JUL-2001; 2001WO-US023642.
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82 rPheSerLeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLe 102

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102 ulleLeuLeuValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGl 122

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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA detecting the level of expression of gene(s) (GS) identified by CAP and the specification, and comparing the expression level to an expression level in an unactivated GC, where a comparing the comparing that a comparing the captesion of at least one gene in GS; (S) screening (M3) GA by contacting GC with an agent that alters the modulating (M2) GA by contacting GC with an agent that alters the capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression in a sample of the disease by detecting the level of expression of the gene is indicative of inflammation; (4) treating configuration (MS) an inflammatory disease, by contacting a tissue having inflammation with an esponse in a subject, exposure of a subject to a pathogen or sterile inflammation in a tissue, an allergic response in a tissue, an allergic response in a tissue, an allergic response in a subject to a pathogen or sterile inflammation (GSPecially chronic) in a tissue, an allergic response in a subject to a pathogen or sterile inflammation (GSPecially chronic) in a tissue, an allergic response in a subject to exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoin injury, renal reperfusion injury, ARDS, adult cardiac reperfusion injury, renal reperfusion injury, sand reperfusion injury, sand respectively bowel disease, Crohn's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                           1866 GGCTTGGGAAAAGTACTGTCAGCGTGTGCCCTACCGTATATTTCCATACATCTAC 1920
122 ulleTrpAlaGluTyrCysLysLeuValProTrpArgileLeuProTyrValTyr 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease;
                                                                                                                                                                                                                                                                                                              Human cDNA differentially expressed in granulocytic cells #435.
                                                                                                                                                                                                                                                                                                                                                          Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; areal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             granulocyte activation; chronic inflammation; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 435; 114pp; English.
                                                                                                                                                       ABK83864 standard; cDNA; 3714 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2001; 2001WO-US030821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2000; 2000US-0237189P.
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GENE-) GENE LOGIC INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200228999-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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30-DEC-2002; 2002US-0436643P

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disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this parent not form part of the printed specification, but was obtained in electronic format directly from MDO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                 82 rPheSerLeuProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1746 GIGGICCCCCCAIGIGGITITAACCACAITCIGCCTIATITCIACAIAAITITATITCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 yAlaAsnLysGlnLysHisValPheLysLysAspProLysAlaProIleTrpGlyLysPr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 ulleLeuLeuValLeuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGl
                                                                                                                                                                                                                                                                                                                                                  51 oProlysValVal------------GlyGlyLysLeuLeuAlaSe
                                                                                                                                                                                                                                                                                                                                                                                               rGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAspLeuLeuLeuAlaLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1866 GGCTTGGGAAAAGTACTGTCAGCGTGTGCCCTACCGTATATTTCCATACATCTAC 1920
                                                                                                                                                                                                                                                   LeuLeuSerGlyLeuAlaAsnLeuCys-IlePheLeuIleGlyTyrLeuValPheArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ane expression profile; hepatotoxicity; liver; toxicity assay; ds.
                                                                                                          Seguence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 3714
67
23
33
16
                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                              (1-3714)
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2002US-0364055P.
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356.50
64.75%
48.20%
47.22%
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ADB56005 standard; DNA; 476
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                  Alignment Scores:
Pred. No.:
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The present invention relates to a method for predicting a toxic effect
of a compound. The method comprises preparing a gene expression profile
of a tissue or call sample exposed to the compound, and comparing the
gene expression profile to a database comprising SEQ ID 1-4925, where
differential expression of the gene indicates at least one toxic effect.
The method is useful for predicting at least one toxic effect of a compound, predicting hepatocoxicity or the progression of a toxic effect.

To a compound, identifying an agent that modulates the onset or
progression of a toxic response, predicting the cellular pathways that a
compound modulates in a cell, and identifying an agent that modulates at
compound modulates in a cell, and identifying an agent that modulates at
compound adulates in a cell, and identifying in contact modulates at
compound activity of a protein. The method and compositions of the
differential expression, are useful in identifying toxicity markers in
liver tissues or cells for drug screening and toxicity markers in
liver tissues or cells for drug screening and toxicity assays. Note: The
sequence date for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                 Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 ArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLys 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 LysValVal------GlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 HisCysAsnTyrLeuGlyAspLeuLeuAlaLeuSerPheSerLeuProCysGlyVal
                                                                 Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 476 BP; 110 A; 119 C; 124 G; 123 T; 0 U; 0 Other;
                                                                 Castle A,
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119
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119
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGTGCCTTACCGAATCATACCGTATGTCTAC 144
                                                                 œ,
                                                                 Higgs
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                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1031; 1156pp; English.
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                                                                   ×
                                                                     Johnson
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70.27%
53.15%
42.58%
                                 (GENE-) GENE LOGIC INC
                                                                 Porter M,
                                                                                                   WPI; 2003-689530/65.
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Best Local Similarity:
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                                                                     Mendrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match:
DB:
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ID AAF2
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Sequence 2481 BP; 471 A; 764 C; 655 G; 589 T; 0 U; 2 Other;
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78. .1505
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Agostino MJ, Steininger
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                                                                                                                                                         ВP
                                                                                           135 IleLeuProTyrValTyr 140
                                                                                                                                                        AAX90448 standard; cDNA; 2481
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99US-00235609.
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CTGCTGCCTGGAATCTTC
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                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-458682/38.
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                                                                                                                                                                                                                                                                                                       Homo sapiens
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20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-1999.
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Treacy M,
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            95
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                                                                                                                                    RESULT 13
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                                                                                                                                                                                                                                                                                                                               The present invention relates to 26 secreted human proteins. The preteins may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate polypeptide expression. For example, they may be used in gene therapy or in vaccines. Typical of diseases which are potentially treatable are cancers (including leukemia), autoimmune diseases, allergies, inflammation, graft rejection, hyperproliferation, cardiovascular diseases (particularly critical limb ischemia and coronary disease) and any involving abnormal angiogenesis, neurodegeneration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               valGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeu 27
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                                                           Secreted protein; gene therapy; vaccine; cancer; leukemia; autoimmune disease; allergy; inflammation; graft rejection; hyperproliferation; cardiovascular; infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                        BP; 351 A; 582 C; 516 G; 444 T; 0 U; 3 Other;
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63
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113
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Mismatches:
Indels:
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Matches:
                                        human secreted protein #13.
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                                                                                                                                                                                                                                                                                                               Claim 1; Page 449-454; 525pp; English.
                                                                                                                                                                                                                               Komatsoulis GA;
                                                                                                                                                                  01-JUN-2000; 2000WO-US015137.
                                                                                                                                                                                     99US-0138625P.
                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                   and/or infectious diseases
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60.96%
43.15%
42.32%
                   (first entry)
                                                                                                                                                                                                                              Ruben SM,
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Best Local Similarity:
                                                                                                                         WO200076531-A1
                                        DNA encoding
                                                                                                     Homo sapiens
                                                                                                                                                                                     11-JUN-1999;
                   27-MAR-2001
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 AAF26559;
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The present sequence encodes a human secreted protein. Human secreted protein polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or amelicrating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, haemacopoises regulating activity, tissue growth activity, activity, chemotactic/chemokinetic activity, and thrombolytic activity, receptor/ligand activity, and thrombolytic activity, receptor/ligand activity, and tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for
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771 TACTICTACATCATCTACATGGCCATCCTGCTCACCGCTGCCTCCGGGACGAGGAC 830
TyrPheTyrProThrTyrLeuLeulleLeuLeuValLeuArgGluArgAgAspGluAla 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, secreted protein, nutrition, cytokine, cell proliferation, differentiation; immune stimulating, vaccine, suppression, gene therapy, hematopoiesis regulation; tissue growth, activin, inhibin, cadherin, chemotactic, chemokinetic; hemostatic; thrombolytic; anti-inflammatory; tumour invasion suppressor; tumour inhibition; ss.
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                                                                                                                                                                       Collins-Racie LA, Merberg D;
RJ, Wong GG, Clark HF, Fechtel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human secreted protein clone pj323_2 nucleotide sequence.
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Clark

Mccoy JM, Lavallie E, Collins-Racie LA, Evans C; Agostino MJ, Steininger RJ, Spaulding V, Wong GG, Merberg D;

2001-639363/73.

Treacy M, A Fechtel K, Jacobs K, Treacy M,

WPI; 2001-639363, P-PSDB; AAU39059

30-MAR-2000; 2000US-00539330. 22-MAR-2001; 2001WO-US009369.

04-DEC-2000; 2000US-00729674 (GEMY) GENETICS INST INC. Secreted human proteins, useful as vaccine for treating various disesuch as autoimmune disorders (e.g. multiple sclerosis), and nervous system disorders (e.g. stroke).

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1065 GTGCAGCTGTCCACCCGCACGCCGTGGGCGTCCTGCTGCTGGGCCTGGTGGCCTACTAC 1124
                                                                                                                                                                                                                                           1365 TACTICTACATCATCATGGCCATCCTGCTGACCCACGCTGCCTCCGGGACGAGCAC 1424
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                                                                                                                                                                                                                                                                                                                                                                          ArgCysSerGlnLysTyrArgGluIleTrpAlaGluTyrCysLysLeuValProTrpArg 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; ss; antiinflammatory; immunosuppressive; nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary; orgostatic; antidiabetic; virucide; antiinfertility; anticonvulsant; vasotropic; antiparkinsonian; immunostimilant; dermatological; antitheumatic; antitumor; antiulcer; osteopathic; tranquiliser; cerebroprotective; oytokine; cell proliferation; cell differentiation; immune deficiency; severe combined immunodeficiency; SCID; tumour; autoimmune deficiency; severe combined immunodeficiency; SCID; tumour; graft-versus-host disease; multiple sclerosis; rheumatoid arthritis; graft-versus-host disease; multiple sclerosis; osteoporosis; osteoporosis; osteoporosis; osteoporosis; periodontal disease; disease; funtification; disease; infection; dardiac disease; gtroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
                                                                                                                                                                                                                ValGluLeuSerLeuLeuSerGlyLeuAlaAsnLeuCysIlePheLeuIleGlyTyrLeu
                                                                                                                                                           28 ValPheArgGlyAlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaPro
                                                                                                                                                                                                                                                                                     GlyAspleuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro
                                                                                                                                                                                                     47 IleTrpGlyLysProProLysValVal--------
                    2481
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                                       Conservative:
Mismatches:
Indels:
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                     Length:
Matches:
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                                                                                             US-10-069-427-6 (1-140) x AAX90448 (1-2481)
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The invention relates to novel human secreted proteins, the nucleic acids encoding them. The protein may exhibit cytokine, cell proliferation or cell differentiation activity or may induce production of other cytokines in certain cell populations and may exhibit immune stimulating or immune suppressing activity, which is useful for the treatment of various immune desorders e.g. severe combined immunodeficiency (SCID), autoimmune disorders e.g. multiple sclerosis, systemic lupus cutoimmune disorders e.g. woulding arthritis, autoimmune pulmonary inflammation.

The proteins are also useful in the treatment of diseases and disorders including tissue, skin and organ transplantation and in graft-versus-host diseases (WTHD), in the induction of tumour immunity, mycloid or lymphoid cutos, incisions and ulcers; as well as in treatment of periodontal disease, disease, disease, whutlington's disease, anylotrophic lateral corrections, and Shy-Drager syndrome, infections, infanction of cardiac and central nervous system vessel e.g. stroke, sepsis, inflammatory disease, bone regeneration. The protein, having activin- or inhibin-related activities is useful as a contraceptive based on the spermatogenesis in male mammals. The proteins and nucleic acids are also contined to the contral as took supplements. The proteins and nucleic acids are also contined to the contraction of secreted activities is useful as sequence encodes a secreted
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Disclosure; Page 552-553; 619pp; English.
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us-10-069-427-6.rng

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1065 GTGCAGCTGTCCACCCCGCACGCCGTGGGCGTCCTGCTGGGGCCTGGTGGGGCTACTAC 1124
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  Fechtel K;
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                    WPI; 2002-040725/05.
P-PSDB; ABB55768.
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                                                                                           1365 TACTICTACATCATCTACATGGCCATCCTGCTGACCCACCGCTGCCTCCGGGACGAGGAC 1424
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                                                                                                                                                                                                                                                               Human, clone bd306-7; clone yb8-1; ATCC number 98599; gene therapy; immune disorder; bacterial infection; fungal infection; cancer; tumour; autoimmune disorder; systemic lupus erythematosus; wound; ulcer; inhibin; osteoporosis; osteoarthritis; nervous system disorder; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; activin; haemophilia; cardiac infarction; stroke; sepsis; arthritis; vulnerary; ischaemia-reperfusion injury; inflammatory bowel disease; chemotactic; crohn's disease; cytostatic; anti-inflammatory; immunomodulator; neuroprotective; haemostatic; thrombolytic; anti-inflammatory; ss.
                                        TyrPheTyrProThrTyrLeuLeuIleLeuLeuValLeuArgGluArgArgAspGluAla 114
  2,4
             GlyAspLeuLeuLeuAlaLeuSerPheSerLeuProCysGlyValSerSerValValPro
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Steininger RJ, Spaulding V;
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Treacy M, Agostino MJ,
                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 141.
                                                                                                                                   1485 CTGCTGCTGGAATCTTC 1502
                                                                                                                                                                                 ABA90946 standard; cDNA; 2481 BP
                                                                                                                       135 IleLeuProTyrValTyr 140
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LAVALLE E R.
COLLINS-RACIE L A
EVANS C.
MERBERG D.
TREACY M.
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20-DEC-1997;
02-JAN-1998;
07-JAN-1998;
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30-MAR-2000;
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22-JAN-1998;
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Merberg D,
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The invention relates to isolated polynucleotides (ABA90876-ABA90968 and ABA908090) and encoded proteins (ABB55809, especially Companies SEQ ID No 19 (ABA90885) and proteins SEQ ID No 19 (ABA90885) and proteins SEQ ID No 20 (ABB55707) contained in proteins SEQ ID No 20 (ABB55707) contained in clones bd306-7 and yb8-1 respectively and the clones bd306-7 and yb8-1 care deposited with the American Type Culture Collection (ATCC) with correspondenties, activity, inmunomodulator, vulnerary, controprotective, activity, inhibin, chemotactic, hamostatic, thrombolytic and anti-inflammatory activity and acting as cytokine modulators, haematopoiesis regulators, tissue growth modulators and/or cadherin and anti-inflammatory activity and acting as cytokine modulators. Companies of the following diseases: immune deficiency and disorders; e.g. bacterial correlations and ulcers, osteoporosis or the following diseases: immune deficiency and disorders; e.g. bacterial crythematosus or graft-versus-host disease; myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or cythematosus or graft-versus-host disease, myeloid or lymphoid cell deficiencies; wound, burns, incisions and ulcers, osteoporosis or conteopathies, e.g. Alzheimer's Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis or Shy-Drager syndrome, hemophila, cardiac inflammatory response syndrome, ischaemia-reperfusion injury, endotoxin lethality, arthitis, inflammatory bowel disease or Crohn's child in dease, or tumours or cancers, pemphigus vulgaris or pemphigus foliaceus
New secreted proteins and encoding polynucleotides, useful in gene therapies, particularly for preventing or treating autoimmune disorders, cancer, graft-versus-host disease, wound, osteoporosis, stroke or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2481 BP; 471 A; 764 C; 655 G; 589 T; 0 U; 2 Other;
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Matches:
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Mismatches:
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¹³⁵ IleLeuProTyrValTyr 140
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1485 CTGCTGCCTGGAATCTTC 1502

Search completed: June 14, 2004, 10:02:16 Job time: 236.291 secs

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1007 107.5 107.5 106.5 106.5 106.5 100.5 1	ESULT 1 Sequence 1, Applicat: Patent No. 6639130: APPLICANT: Jang, Jy APPLICANT: Sheen, Jq TITLE OF INVENTION: FILE REFERENCE: 0074 CURRENT APPLICATION CURRENT APPLICATION ERALIER APPLICATION ERALIER APPLICATION ERALIER FILING DATE SALIER FILING DATE SOFTWARE: FALIER APPLICATION ERALIER FILING DATE SOFTWARE: FALIER FORES SOFTWARE: FALIER FILING-BATE SEQ ID NO. ERALIER FILING-BATE SEQ ID NO. TYPE: RALIER FALIER FALIER TYPE: RALIER FALIER FALIER TYPE: RALIER FALIER FA	Ouery Match Best Local Signatures 2922 Matches 2922 Matches 2922 Matches 2921
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                                                                                                  Sequence 4, Application US/09342653
Patent No. 6306632
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION: Chromatin Associated Proteins
FILE REPERENCE: BB-1118
CURRENT APPLICATION WUMBER: US/09/342,653
CURRENT APPLICATION NUMBER: 60/092,841
BARLIER APPLICATION NUMBER: 60/092,841
BARLIER FILING DATE: 1999-06-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
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Sequence 7, Application US/09342653
Sequence 7, Application US/09342653
Settle No. 636652
SEAPLICANT: Cahoon, Rebecca E.
APPLICANT: Catalaski, Antoni
TITLE OF INVENTION: Chromatin Associated ProfILE REFERENCE: BB-1118
CURRENT APPLICATION NUMBER: US/09/342,653
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: 60/092,841
EARLIER FILING DATE: July 14, 1998
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Microsoft Office 97
SEQ ID NO 7
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361 PWRILPYV 368
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-342-653-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-342-653-7
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US-09-342-653-7
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110 ALLVGLGMSAG-LPLGALPEMLIPLAFVATLTAFIFSLFLYM---KAQVAPVSALAPGGN 165
                                                                                                                             SGNLIHDWWFGIQLNPQFMGID-----LKAGMMGWLLINLSILMKSIQ-DGTLSQSMIL 179
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PARENE NO. 14

Sequence 9, Application US/08879337B

Sequence 9, Application US/08879337B

Sequence 9, Application US/08879337B

SEQUENCE SEQU
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Best Local Similarity 38.5%; Pred. No. 2e-56;
Matches 145; Conservative 65; Mismatches 127; Indels
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350 REIWAEYRKLVPW 362
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SEQ ID NO 8
LENGTH: 637
TYPE: PRT
ORGANISM: Gallus domesticus
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APPLICANT: Jang, Jyan-Chyun
APPLICANT: Sheen, Jen
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                                                             US-08-879-337-8
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                                                                                                                                                                                                                                                                                                                                                                                       Length 424;
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APPLICANT: Jang, Jyan-Chyun
APPLICANT: Sheen, Jen
TITLE Sheen, Jen
TITLE SPERENCE: 00786/33801
CURRENT APPLICATION WHOREN: US/08/879,337B
CURRENT FILING DATE: 1997-06-20
BARLIER APPLICATION NUMBER: 60/022,086
BARLIER FILING DATE: 1996-06-21
SUMMER OF SEQ ID NOS: 24
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                        AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.3%; Score 575.5; DB 4; Best Local Similarity 36.1%; Pred. No. 5e-51; Matches 137; Conservative 68; Mismatches 137;
                                                                                                                                   APPLICANT: Jang, Varn-Chyun
APPLICANT: Sheen Jen
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND
FILE REFERENCE: 00786/338001
CURRENT APPLICATION NUMBER: US/08/979,337B
CURRENT APPLICATION NUMBER: 60/022,086
EARLIER APPLICATION NUMBER: 60/022,086
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Schizosaccharomyces pombe
US-08-879-337-5
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Sequence 8, Application US/08879337B
Patent No. 6639130
GENERAL INFORMATION:
                                                                                          Sequence 5, Application US/08879337B Patent No. 6639130
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599 WEKYCQRVPYRIFPYIY 615
                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                            | | | | : : | | | | : | | | | : | | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                     LOALTPSWNS----VPLLVGFFTYLAVAGSILP-GKLVPGVALLDGTRLHYCCNGLLSLL
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CURRENT APPLICATION UNMERS: US/08/879,337B
CURRENT FILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 60/022,086
EARLIER FILING DATE: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 4
Length 637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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28.0%; Score 549.5; DB 4;
Best Local Similarity 34.3%; Pred. No. 2.6e-48;
Matches 133; Conservative 76; Mismatches 136;
Query Match
28.9%; Score 568; DB 4; L
Best Local Similarity 37.3%; Pred. No. 5.2e-50;
Matches 139; Conservative 65; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08879337B Patent No. 6639130
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COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,674
FILING DATE: May 15, 1995
CLASSIFICATION BATA:
APPLICATION DATA:
APPLICATION WUMBER: US/08/107,347
FILING DATE: AUGUSE 16, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                         ; DATE: 1990
; RELEVANT RESIDUES IN SEQ ID NO:
US-08-439-131A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 AEKYREIWAEYRKLVPW 362
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                                                                                                                                                                    Query Match 27.9%;
Best Local Similarity 36.1%;
Matches 136; Conservative 6
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             PAGES: 1535-1542
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STATE: Ne
COUNTRY:
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                                                                                                                                                                                                                              PFSFSIQGWWLLMNSVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPIWGKPP 281
                                                                                                                                                                                                                                                                KVIGGKLLASGYWGIARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRERTD 341
                                                                                                   163 ILMKS-IQDGTLSQSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Worman, H. J.
AUTHORS: Blobel, G.
AUTHORS: Blobel, G.
TITLE: The Lamin B Receptor of the Nuclear Envelope
TITLE: Inner Membrane
TOURNAL: J. Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08439131A
Patent No. 5512472
GENERAL INCRMATION:
APPLICANT: Lai, Margaret H. K.
APPLICANT: Bard, Martin
APPLICANT: Bard, Martin
APPLICANT: Arisch, Donald R.
TILLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
Patent No. 5512472
TITLE OF INVENTION: Reductase
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/439,131A
FILLING DATE: 11-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :| | | | | | | | EHKCRLKYGENWEEYERKVPYKIIPYVY 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 85,
REFERENCE/DOCKET UNBER: 85,
TELECOMMUNICATION:
TELEPHONE: 201-831-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 419 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One Cyanamid Plaza
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MEDIUM TYPE: Floppy
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: U.S.A.
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ZIP: 07470
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US-08-439-131A-3
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50 LPALESLWETKVFGVFLLWFFFQALFY---LLPIGKVVFGLPLSNPRKPQYRINGFYAFL 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 LSQSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSF81QGWWL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 PSLSMILVNSFQLLYVVDALWNEBAVLTTMDITHDGFGFMLAFGDLVWVPFVYSLQAFYI 279
                                                                                                                                                                                                                                                                                               67 LLVA----LLGIGAKWGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGSSL 122
                                                                                                                                                                                                                                                                                                                                                                                                             123 KP-HLSGNLIHDWWFGIQLNPQFMGIDLK-----AGMMGWLLINLSIL---MKSIQDGT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 GKLLASGYWGIARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRERTDEARC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 LMNSVELT----PAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAP---IWGKPPKVIG
                                                                                                                                                                                      12 LQALIPSWNS----VPLLVGFFTYLAVAGSILP-GKLVPGVALLDGTRLHYCCNGLLSLL
                                                                                                                                     40; Gaps
                                                                                 Length 419;
                                                                              ; Score 549; DB 1; Length 419
; Pred. No. 2.7e-48;
69; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-440-674-2

| Sequence 2, Application US/08440674
| Patent No. 5555496
| Patent No. 5555496
| TILLE OF INVENTION: A DNA Sequence Encoding Sterol Patent No. 5555496
| TILLE OF INVENTION: 14
| TILLE OF INVENTION: Reductase | VUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: American Cyanamid Company STREET: One Cyanamid Plaza
3: FROM 190 TO 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Alan M. Gordon
REGISTRATION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-P0012 DIV (32,141)
TELECOMMUNICATION INFORMATION:
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66 ILLIVALLGIGAK------MGFVSPTAISDRGLELLSTTFAFSFLVT-----LIL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 ILMKS-IQDGTLSQSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWI 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPSFSIQGWWLLMMSVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKKNPKAPIWGKPP 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          292 PFTYSLQARYLSVSPVELGWVKVVGILAIMFLGFHIFHSANKQKSRFRQGKLENLKSIQT 351
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27.9%; Score 547.5; DB 1; Length
Best Local Similarity 34.3%; Pred. No. 4.1e-48;
Matches 133; Conservative 76; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08440674;
Patent No. 5525496;
GENERAL INFORMATION:
APPLICANT: Margaret H. Lai
TITLE OF INVENTION: A DNA Sequence Encoding Sterol
                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,131A
FILING DATE: 11-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                854-012 (32,141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      342 EARCAEKYREIWAEYRKLVPWRILPYVY 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | :| || | | | | : ||::|||||| 
EHKCRLKYGENWEEYERKVPYKIIPYVY 438
ADDRESSEE: American Cyanamid Company
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              30,637
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gordon, Alan M.
REGISTRATION NUMBER: 30,637
REFERENCE/DOCKET NUMBER: 85-
TELECOMMUNICATION INFORMATION:
                   One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 WNSV-PL--LVG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201-831-3244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201-831-3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                           New Jersey
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
        STREET: Wayne
                                                                                                07470
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US-08-440-674-5
                                                                              COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 VGHPIAISWPVAAAITILNC----İGYXIFRSANSOKONFRRNFADPKLSYLKVIPTATG 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 GKLLASGYWGIARHCNYLGDIMLALSFSLPCGISSPIPYFYPIYLLILLIWRERTDEARC 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 LPALESLWETKVFGVFLLWFFFQALFY---LLPIGKVVEGLPLSNPRKPQYRINGFYAFL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LLVA----LLGIGARMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGSSL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 KP-HLSGNLIHDWWFGIQLNPQFMGIDLK-----AGMNGWLLINLSIL---MKSIQDGT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 LSQSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWL 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 LMNSVELT----PAALVANCEVFLIGYMVFRGANKQKHVFKKNPKAP---IWGKPPKVIG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LOALTPSWNS----VPLLVGFFTYLAVAGSILP-GKLVPGVALLDGTRLHYCCNGLLSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Lai, Margaret H. K.
APPLICANT: Bard, Martin
APPLICANT: Brisch, Monaid R.
TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
Patent No. 5512472
TITLE OF INVENTION: Reductase
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.9%; Score 549; DB 1; Length 41 36.1%; Pred. No. 2.7e-48; ive 69; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                             TITLE: (excerpt): The Lamin B Receptor of the TITLE: Nuclear Envelope Inner Membrane JOURNAL: Journal of Cell Biology VOLUME: 111 PAGES: 1535-1542
PAGES: Sequence set out in Figure 5, page 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 to 608
                                                                                                                                                                                                                               NAME/KEY: chicken
NAME/KEY: nuclear lamin B receptor
PUBLICATION INFORMATION:
AUTHORS: H.J. Worman, C.D. Evans, and G.
AUTHORS: Blobel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08439131A Patent No. 5512472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELEVANT RESIDUES IN SEQ ID NO:
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                                                                                                                                                               MOLECULE TYPE:
DESCRIPTION: polypeptide
FEATURE:
      TELEFHONE: 201-831-3244
TELEFA: 201-831-3305
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 36.19
Matches 136; Conservative
                                                                                     LENGTH: 419 residues
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 5525496
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Gaps

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352 K-RGTKLLCDGWWAKSQHINYFGDWLISLSWCLATWFQTPLTYYYSLYFATLLLHRQQRD 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 LSLLLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGSSL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 KPHLSGNLIHDWWFGIQLNPQF-MGIDLKA-----GMMGWLLINLSILMKSIQD-GTLS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 --GSSGNLIIDFYWGMELYPRIGKHFDIKVFTNCRFGMMSWAVLALTYCIKQYEENGKVA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 DSMLVNTALMLVYVTKFFWWEAGYWSTMDIAHDRAGFYICWGCLVWVPSVYTSPGMYLVN 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 QSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 --GGK-----LLASGYWGIARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LQAL----TPSWNSVPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCNGL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235 N----SVELTPAAIVANCFVFLIGYMVFRGANKQKHVFKK-NPKAPIWGKPPKVI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338 ERTDEARCAEKYREIWAEYRKLVPWRILPYVY 369
                                                                                                                                                                                                                                    APPLICANT: Famodu, Omolayo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TILE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2.2. Application US/09443041A
Batent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
                                       342 EARCAEKYREIWAEYRKLVPWRILPYVY 369
                                                              CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
                                                                                                                                                                           Sequence 20, Application US/09443041A
Patent No. 6465717
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Glycine max
US-09-443-041A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                        US-09-443-041A-20
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US-09-443-041A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163 ILMKS-IQDGTLSQSMILYQLFCALYILDYFVHEBYNTSTWDIIAERLGFMLVFGDLVWI 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 WNSV-PL--LVG-----FFTYLAVAGSILPGKLVPGVALLDGTRLHYCCNGLLSL 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.9%; Score 547.5; DB 1; Length 438; 34.3%; Pred. No. 4.1e-48; Live 76; Mismatches 136; Indels 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DESCRIPTION: polypeptide
FRAGMENT TYPE: entire sequence
LIMMEDIATE SOURCE: Saccharomyces cerevisiae
IMMEDIATE SOURCE: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: American Cyanamid Company
One Cyanamid Plaza
                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,674
FILING DATE: MAY 15, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: ANGUER 16, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan M. Gordon
REGISTATION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-P0012 D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: translated polyOTHER INFORMATION: sterol 14
COTHER INFORMATION: reductase gene
US-08-440-674-5
              14
Reductase
                                                                                                                                                                                                                                  MEDIUS.
COMPUTER: IBM ...
OPERATING SYSTEM: MS DUS
TOTAL MOTE PROCESSOR
TOTAL MOTE PROCESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 438 amino acids
amino acid
        TITLE OF INVENTION: 14
TITLE OF INVENTION: Redu
VMDER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.3
Matches 133; Conservative
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                                                                                                                                                  New Jersey
: USA
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                                                                                                                                              STATE: New COUNTRY: US ZIP: 07470
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52 VOGLINIWPR-PTLIAWKIIFCYGAFEAILQLLLPGKRVEGPISPAGNRPVYKANGLAAY 110
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                                                                                                                                                                                                                                                               DNA sequence coding for a protein of A, thaliana having a delta-5,7 sterol,delta-7 reductase activity, delta7-Red protein, production process, strains of transformed yeasts, uses.
                                                                                                        110 UTLITYLSLM-WFGIFNPAIUYDHLGEIXSALUFGSFUFCIFLXIKGHLAPSSSDS---G 165
                                                                                                                                                         126 LSGNLIHDWWFGIQLNPQF-MGIDLKA-----GMMGWLLINLSILMKSIQ-DGTLSQSM 177
                                                                                                                                                                                  178 ILYQLFCALYILDYFVHEEYMISTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWLLMNSV 237
                                                                                                                                                                                                                                                                                                                                           286 NLGPQLALSILLAGILCIXINY----DCDRQRQEFRRINGKCSIWGKAPSKIVASYQTIN 341
                                                                                                                                                                                                                                                                                                                                                                                                     ----GGKLLASGYWGIARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLINRERT 340
                                                                                                                                                                                                                                                                                                                                                                                                                          342 GETKSSLLLTSGWWGLSRHFHYVPEILSAFFWTVPALFDHFLFYFYVIFUTLLLFDRAKR 401
                         12 LOALTPSWNSVPLLVG-----PFTYLAVAGSILPGKLVPGVALLDGTRLHYCCNGLLSL
LQALTP----SWNSVPLLVGFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCNGLLS-L
                                                                              LLLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSGCKSQSKGSSLKPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
                                                                                                                                                                                                                                                                                                                        238 ELTP----AAIVANCFVFLIGYMVFRGANKOKHVFKK-NPKAPIWGKPPKVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.1%; Score 415.5; DB 1;
29.7%; Pred. No. 1.7e-34;
tive 78; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               341 DEARCAEKYREIWAEYRKLVPWRILPYVY 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,435
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA sequence
TITLE OF INVENTION: of A, thalian
TITLE OF INVENTION: reductase at
TITLE OF INVENTION: process, stri
NUMBER OF SEQUENCES: 31
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9501723
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9506517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08601435 Patent No. 5759801 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 01-UN-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-435-2
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Best Local S:
Matches 116,
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                                                                                                                                                                                                                                                                                                                                                                               233 LMNSVELTP----AAIVANCFVFLIGYMVFRGANKOKHVFKK-NPKAPIWGK-PPKVIG- 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LILLVALLGIGAKMGFVSPTAISDRGLELLSTTFAFSFLVTLILHFSG---CKSQSKGS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLKPHLSGNLIHDWWFGIQLNPQF-MGIDLKA-----GMMGWLLINLSILMKSIQ-DGT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 LSQSMILYQLFCALYILDYFVHEEYMTSTWDIIAERLGFMLVFGDLVWIPFSFSIQGWWL 232
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                                                                                                                                                                                                                                                                                                                                                  11 LLQALIPSWNSVPLLV----GFFTYLAVAGSILPGKLVPGVALLDGTRLHYCCNGLLS
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                                                                                                                                                                                                                                                                       Length 450;
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                                                                                                                                                                                                                                                                     / Match 22.5%; Score 441.5; DB 4; Local Similarity 29.7%; Pred. No. 3.8e-37; Nes 117; Conservative 79; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WRERTDEARCAEKYREIWAEYRKLVPWRILPYVY 369
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Sequence 18, Application US/09443041A

GENERAL INFORMATION:

APPLICANT: Famedu, Cmolayo O.

APPLICANT: Famedu, Cmolayo O.

APPLICANT: Rafalski, Antoni

APPLICANT: Shen, Jennie

TITLE OF INVENTION: Sterol Metabolism Enzymes

FILE REFERENCE:

CURRENT APPLICANTON NUMBER: US/09/443,041A

CURRENT FILING DATE: 1999-11-18

PRIOR APPLICATION NUMBER: 60/109,283

PRIOR FILING DATE: 1998-11-20

NUMBER OF EXQ ID NOS: 33

SOFTWARE: Microsoft Office 97

SEQ ID NO 18
                           CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR PILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 22
LENGTH: 450
                                                                                                                                                                                             TYPE: PRT ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 22.1
Best Local Similarity 29.0
Matches 113; Conservative
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ORGANISM: Oryza sativa
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US-09-443-041A-18
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                 FILE REFERENCE
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Matches
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177 MILYQLPCALYILDYFVHEBYMTSTWDITAERLGFMLVFGDLVWIPPSFSIQGWWLLMNS 236
                                                                                                                              286 -----GKLLASGYWGIARHCNYLGDLMLALSFSLPCGISSPIPYFYPIYLLILLIWRER 339
                                                                                                                                         343 SGETKTSLLLTSGWWGLARHFHYVPEILSAFFWTVPALFDNFLAYFY--VLTLLLFDRAK 400
                                                                                                                                                                340 TDEARCAEKYREIWAEYRKLVPWRILPYVY 369
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401 RDDDRCRSKYGKYWKLYCEKVKYRIIPGIY 430
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Search completed: June 14, 2004, 14:42:12 Job time: 25.6483 secs

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Perfect score:

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Scoring table: Sequence:

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Sequence 17, Appl Sequence 23, Appl Sequence 19, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 46, Appli Sequence 21, Appl Sequence 71, Appl Sequence 21, Appl Sequence 2, Appli Sequence 3678, Appl Sequence 3678, Appli Sequence 3678, Appli Sequence 1, Appli Sequence 11818, A Sequence 11818, A Sequence 1184, A Sequence 1184, A Sequence 372, Appli Sequ
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Sequence 3, Appli
Sequence 5, Appli
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US-09-342-653-3
; Sequence 3, Application US/09342653
; Sequence 3, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION UNMERR: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER APPLICATION NUMBER: 60/092,841
; MUMBER OF SEQ ID NOS: 7
; SEQ ID NO 3
; SEQ ID NO 3
US-09-443-041A-17

US-09-443-041A-19

US-08-943-201-1

US-08-931-047-1

US-08-931-047-1

US-08-931-381-463

US-09-833-381-463

US-09-833-381-464

US-09-833-381-464

US-09-103-8449-71

US-09-133-381-464

US-09-133-381-464

US-09-133-381-464

US-09-133-381-464

US-09-133-381-1884

US-09-133-381-1888

US-09-132-991A-1888

US-09-132-991A-11888

US-09-132-991A-37-3

US-09-133-75-4

US-08-138-17-1

US-08-138-17-1

US-08-138-17-1

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US-08-138-17-1
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Matches:
Conservative:
Mismatches:
Indels:
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638.00
91.91%
82.35%
       32.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18.7 | 18
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; ORGANISM: Oryza sativa
US-09-342-653-3
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Best Local Similarity:
Query Match:
DB:
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-MODEL=frame+ pan.model_-DEV=xlh
-Q=/cgn2_1/USFOC_SPOOl/US10069427/runat_14062004_104801_24788/app_query.fasta_1.846
-Q=/cgn2_1/USFOC_SPOOl/US10069427/runat_14062004_I04801_24788/app_query.fasta_1.846
-DB=ISSUGG_PATENTS_DEVERTS_1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR_SCORE_CT_TRR_MINSO -ALIGN=15
-LIST=45 -DOCALIGN=200 -TRR_SCORE_CT_TRR_MAX=100 -TRR_MINSO -ALIGN=15
-USFR=US1069427_GCN_1 1 76 @runat_14062004_104801_24788 -NCPU=6 -ICPU=3
-NO MWAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
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-ICR_ARRED -LONGLOG -LONGRAPEXT=0.5 -DELORD=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 10, Appli
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11. /GGT2_6/ptodate/2/ina/5A_COMB.seq:*
12. /GGT2_6/ptodate/2/ina/5B_COMB.seq:*
3: /GGT2_6/ptodata/2/ina/6A_COMB.seq:*
4: /GGT2_6/ptodata/2/ina/6B_COMB.seq:*
5: /GGT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /GGT2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                           ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeulleLeuLeullell
                                                                                                   106 ValleuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla
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 APPLICANT: Jang, Jyan-Chyun
APPLICANT: Jang, Jyan-Chyun
APPLICANT: Sheen, Jen
TITLE OF INTENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REPERBUCE: 00786/33801
CURRENT PILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 00/022,086
EARLIER APPLICATION PUMBER: 096-06-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO | SEQ ID NO |
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
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| Sequence 2, Application US/08879337B |
| Patent No. 6639130 |
| Patent No. 6639130 |
| Patent No. 6639130 |
| PAPLICANT: Jang, Jyan-Chyun |
| APPLICANT: Shear, Jen |
| TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF |
| TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF |
| CURRENT PILING DATE: 1997-06-20 |
| PARLIER PILING DATE: 1996-06-21 |
| NUMBER OF SEQ ID NOS: 24 |
| SOFTWARE FREING FOR Windows Version 4.0 |
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; OTHER INFORMATION: N can be any US-08-879-337-2
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                                                                                                     5421 TAAGTICIGAGACAIGGGGITAITIICCAIICITACAIAICIACACAAACCCACIA 5480
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; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; TILE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: B8-1118
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFFWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Triticum aestivum
US-09-342-653-5
                                                                                                                                                 60 uAlaSerGlyTyrTrp
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LENGTH: 572
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US-09-342-653-5
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                         uargargaspelualaargcysSerGlnLysTyrargeluileTrpAlaeluTyrCysLy 129
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                                                               yAspleuLeuAlaLeuSerPheSerLeuProCysGlyVal-----
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Patent No. 6639130

GENERAL INFORMATION:

APPLICANT: Jang, Jyan-Chyun

APPLICANT: Jenen, Jen

TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF

FILE REFERENCE: 00786/338001

CURRENT APPLICATION NUMBER: US/08/879,337B

CURRENT FILING DATE: 1997-06-20

EARLIER APPLICATION NUMBER: 60/022,086

EARLIER FILING DATE: 1996-06-21

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 3
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: N can be any nucleotide.
US-08-879-337-3
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ORGANISM: Arabidopsis thaliana
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Best Local Similarity:
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Pred. No.:
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                                                                 Sequence 71, Application US/09221298
Patent No. 6284241
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER
FILE REPERSINCE: 210121.471
CURRENT APPLICATION NUMBER: US/09/221,298
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 71
LENGTH: 428
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Matches:
Conservative:
Mismatches:
Indels:
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; OTHER INFORMATION: Where n is a,
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                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: modified_base
LOCATION: (281)
OTHER INFORMATION: Where n is a,
FEATURE:
LOCATION: (308)
OTHER INFORMATION: where n is a,
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LOCATION: (403)
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NAME/KEY: modified_base
LOCATION: (376)
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NAME/KEY: modified_base
LOCATION: (364)
OTHER INFORMATION: Where
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LOCATION: (397)
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NAME/KEY: modified_base
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Best Local Similarity:
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US-09-221-298-71/c
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US-09-342-653-1
; Sequence 1, Application US/09342653
; Sequence 1, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cathoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins; FILE REFERENCE: BB-1118
; CURRENT RAPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; BARLIER PILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOCFWARE: Microsoft Office 97
    Length:
Matches:
Conservative:
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Query Match:
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; ORGANISM: Zea mays
US-09-342-653-1
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TYPE: nucleic acid
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APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrists, Heather
APPLICANT: Becrists, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Benson, Darin R.
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121-4712.
CURRENT APPLICATION NUMBER: US/09/401,064
CURRENT FILING DATE: 1999-09-22
NUMBER OF SEQ ID NOS: 371
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 71
LENGTH: 428
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                                                       86 ProCysGlyValSerSerValValProTyrPheTyrProThrTyrLeuLeulleLeuleu 105
                                                                                                                               106 ValleuArgGluArgArgAspGluAlaArgCysSerGlnLysTyrArgGluIleTrpAla 125
260 GGCTTTGTTGGCCACCCAATTACTTGGGTGATCTCATCATGGCCTTGGCGTGGTCCTC 201
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                                                                            49 Gly-----LysProProLysValValGlyGlyLysLeu---LeuAlaSerGlyTyrTrp
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Mismatches:
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Gaps:
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Patent No. 6623923
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US-09-401-064-71
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                 RESULT 8
US-09-401-064-71/c
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Query Match:
DB:
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                                                                                     ------GlyGlyLysLeuLeuAla 61
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Fatent No. 5525496
GENERAL INFORMATION:
APPLICANT: Margaret H. Lai
TITLE OF INVENTION: 14
TITLE OF INVENTION: 14
TITLE OF INVENTION: 14
TITLE OF INVENTION: 14
TITLE OF INVENTION: 16
TITLE OF UNCENTION: 16
TITLE OF U
1397 ATCTTCCACTCGGCAAATAAGCAAAAATCTGAGTTTAGACAA--
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APPLICATION NUMBER: US 08/107,347
APPLICATION NUMBER: US 08/107,347
FILING DATE: August 16, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan M. Gordon
REGISTRATION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
TELECOMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
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OTHER INFORMATION: sterol 14 reductase gene,
OTHER INFORMATION: translated
                                                                                48 TrpGlyLysProProLysValVal------
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,674
FILING DATE: May 15, 1995
CLASSIFICATION: 536
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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1337 GTGGAATTGGGATGGGTGAAAGTTGTCGGTATATTAGCCATAATGTTTTGGGTTTCCAC 1396
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Patent No. 5591570
Patent No. 5591570
Patent No. 559170
APPLICANT: Margaret H. Lai
APPLICANT: Martin Bard
APPLICANT: Donald R. Kinsch
TITLE OF INVENTION: Sterol Delta 14 Reductase Screen
OTHER INFORMATION: polypeptide and flanking DNA
                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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NAME: Alan M. Gordon
REGISTRALION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-010 (32,141)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REPABLE FORM:
MEDIUM TYPE: 5.25" 360 Kb diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,348
FILING DATE: 19930816
CLASSIFICATION: 435
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
ADDRESSEE: Patent Law Department
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COUNTRY: United States
ZIP: 07470
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Query Match:
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Best Local Similari
                                                                   Alignment Scores:
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STATE: Ne
COUNTRY:
    US-08-440-674-1
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|1016 CTTCTAGCTGGAATG----TTGTGCATATAC---ATAAACTAT------GAT 1054
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Matches:
Conservative:
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Facent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famedu, Omclayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
TITLE OF INVENTION Sterol Metabolism Enzymes
FILE REFERENCE:
GURRENT APPLICATION UNMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-16
FRIOR PRILICATION NUMBER: 60/109,283
FRIOR PRILING DATE: 1999-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
TEMPLY APPLICATION 17
                                                                                                                                                                                                                            US-10-069-427-6 (1-140) x US-09-443-041A-21 (1-1695)
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                                 TYPE: DNA
ORGANISM: Triticum aestivum
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ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
DB:
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US-09-443-041A-17
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Pred. No.:
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                                                                   US-09-443-041A-21
SEQ ID NO 21
LENGTH: 1695
                                                                                                  Alignment Scores:
Pred. No.:
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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Patent No. 6465717
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Famedu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennel
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
     TELERAX: 201-831-3244
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 2528 bases
TYPE: nucleic acid
STRANDENESS: double
FOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: DNA encoding a polypeptide
FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: Saccharomyces cerevisiae
IMMEDIATE SOURCE: clone
                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-069-427-6 (1-140) x US-08-107-348-1 (1-2528)
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CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
SUFFRER SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
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Best Local Similarity:
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LysValGluLeuSerLeuLeu---SerGlyLeuAlaAsnLeuCysIlePheLeuIleGly 25
                                                                                                                                                                                   1151 TATGTCCCTGAAATACTGGCAGCTTTCTTCTGGACAGTCCCAGCTCTTTTCGAACATTTT
                                                                                                             45 AlaProlleTrpGlyLysProProLysValVal....------GlyGly ...
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APPLICANT: Sheen, Jen.
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
TITLE OF INVENTION: PLANT STEROL REDUCTASES AND USES THEREOF
FILE REPERENCEN: 00766/338001
CURRENT APPLICATION NUMBER: US/08/879,337B
CURRENT FILING DATE: 1997-06-20
EARLIER APPLICATION NUMBER: 60/022,086
EARLIER PILICATION NUMBER: 1996-06-21
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Arabidopsis thaliana
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1044 TGTGATCGTCAGCGCCAAGAATTCCGTCGGACAAATGGGGAAATGCTCAATATGGGGCAAA 1103
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                                                                                                                                                                    32 AlaAsnLysGlnLysHisValPheLysLys---AspProLysAlaProIleTrpGlyLys 50
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Matches:
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; Sequence 19, Application US/09443041A
; Patent No. 64651T;
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT APPLICATION NUMBER: 60/109,283
; CURRENT FILING DATE: 1999-11-18
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 1646
                                                                                  US-10-069-427-6 (1-140) x US-09-443-041A-17 (1-1870)
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|404 ATTTAC 1409
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          Percent Similarity:
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121 CTTGTCCCCTGGAGAATACTTCCTTATGTTTAT 153

Search completed: June 14, 2004, 12:20:38 Job time: 45.8821 secs

Soybean s Candida a Sterol-de Saccharom Saccharom

Gene LBR Human cDN

Human ova Human sec Human cDN Human pol Human Del Human Del

Primary r Human REM Aspergill Aspergill Aspergill Aspergill Aspergill CDNA enco CDNA e

Gene #107 cDNA enco Colon tum

Aspergil]

us-10-069-427-8.rng

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Run on:

Sequence:

Searched:

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Abk83864
Abz130676
Abz130676
Abz130672
Abz13012
Abz13012
Abz142
Abz13012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Soybean sterol delta-14 reductase clone ssm.pk0031.d12:fis.
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AAX23387
ABA52386
ADB53021
ADB53021
ABT20861
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ABT2867
AAT28630
ABX18830
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                  Kinney AJ;
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-MCDEL=frame+ p2n.model -DEV=xlh
-Q=/cgp2 1/USFDC spool/US10069427/runat 14062004 104800 24751/app query.fasta_1.846
-DB=N Geneseq_29Jan04 -QFWT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -IAMTRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-NODE=LOCAL -OUTFWT=pto -NOTMS=ext -HEARSIZE=500 -MINIEN=0 -MAXIEN=200000000
-USER-USB-LOOPCR=1 - SEG Grunat 14062004 104800 24751 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                         US-10-069-427-8
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1 MMESHVDLGFLLQALTPSWN.....REIWAEYRKLVPWRILPYVY 369
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      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                               nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Famodu 00, Kinney AJ
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                                                                         The present sequence is that of the full insert sequence of clone ssm.pk0031.d12, which includes a full-length coding region for soybean sterol delta-14 reductase (see AAB20381). The clone was isolated from a sterol delta-14 reductase (see AAB20381). The clone was isolated from a predicted protein shows anno acid sequence homology to Arabidopsis thaliana and Ascobolus immersus sterol delta-14 reductases. The invention relates to isolated polymucleotides encoding sterol delta-14 reductases and to transgenic plants comprising such polymucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the sterol delta-14 reductase, in sense or antisense orientation, where sterol delta-14 reductase genes will provide a means of alterial sterol composition of plants. Compounds that may be useful as novel herbicides and fungicides, and to identify mutants of these genes that are resistant to these herbicides and will enable the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase.
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                                                           Claim 7; Page 39; 45pp; English.
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WPI; 2001-266146/27
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                                                                            ThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrp
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GlnLeuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corn sterol delta-14 reductase clone p0097.cgrau67ra:fis.
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                                 TCAATGATTCTCTACCAGCTATTCTGTGCACTATACATCCTGGACTATTTGTACATGAA
                                                                                                     GluTyrWetThrSerThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis C-14 sterol reductase cDNA clone D13.
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                                                                                                                                                                     The present sequence is that of the full-insert sequence of clone p0097.cgrau67za:fis, coding for corn sterol delta-14 reductase (see AAB20379). The clone was isolated from a cDNA library prepared from corn v9 whorl section + ECB1, following database homology searches. The predicted polypeptide shows amino acid sequence homology to Arabidopsis thaliana and Ascobolus immersus sterol delta-14 reductases. The invention of relates to isolated polymulecides encoding sterol delta-14 reductases and to transgenic plants comprising such polymulecides. It also relates to the construction of a chimmeric gene encoding all or a portion of the sterol delta-14 reductase, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell. The availability of plant sterol delta-14 reductase genes will provide a means of altering sterol production and/or composition of plants, to identify compounds that may be useful as novel herbicides and fungicides, and to identify mutants of these genes that are resistant to these herbicides and will enable the composition of herbicides and will enable the
                                                 Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase.
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New isolated plant C-14 sterol reductase gene - used to develop products for the genetic manipulation of a plant sterol biosynthetic pathway to improve plant characteristics.
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Claim 7; Fig 14; 71pp; English

(see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra cond state) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra cond life), that displayed a life span that was at least 3 times graater then wild-type plants, was isolated. The ell mutant was isolated by T-DNA tagging, and used to screen cDNA and genomic libraries from a wild-type plant to identify clone D13 and a 6588 by genomic clone (see AAV04238). A pure plant C-14 sterol reductase (C145R) is claimed, as are purified DNA encoding C145R, a vector, a method of producing recombinant C145R using transformed plant cells, a transgenic plant that expresses C145R DNA and a seed or cell from such a plant, and methods for detecting and isolating a seed or cell from such a plant, and methods for detecting and isolating a c145R gene, and for reducing the level of C145R in a transgenic plant composition is useful for improving food quality and oil stability, and composition is useful for improving food quality and oil stability, and correquenties. Reduced production of C145R can increase the life-span of plants and produce plants having reduced and more compact proportions. Overproduction is useful for enhancing the production of medically or agriculturally useful steroid compounds. C145R polypeptides are also useful for the development of enzyme inhibitors of the sterol

Sequence 1429 BP; 369 A; 269 C; 305 G; 481 T; 0 U; 5 Other;

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905-01287149 905-01287149 905-01300775 905-01306109 905-01306109 905-01324089 905-01324689 905-01324689 905-01324689	99US-0132863P. 99US-0134286P. 99US-0134219P. 99US-0134219P. 99US-0134708P. 99US-0134708P. 99US-0135124P. 99US-0135124P. 99US-0135124P. 99US-0135124P. 99US-0135128P. 99US-0135128P. 99US-0137528P. 99US-0137528P. 99US-0137528P. 99US-0137528P. 99US-0137528P. 99US-0137528P. 99US-0137528P.	9016-0139452P 9018-0139453P 9018-0139458P 9018-0139458P 9018-0139458P 9018-0139458P 9018-0139458P 9018-0139461P 9018-0139463P 9018-0139463P 9018-0139463P 9018-0139463P 9018-0139463P 9018-0139463P 9018-0139463P 9018-013963P 9018-013963P	015-01412878 015-01418428 015-01418428 016-01420558 018-01420558 018-01420558 018-01420558 018-01420558 018-01440658 018-01440868 018-01440868 018-01440868
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         IlepropheSerpheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThr
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      GluTyrMetThrSerThrTrpAspIleIleAlaGluArgLeuGlyPheMetLeuValPhe
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294
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Matches:
Conservative:
Mismatches:
Indels:
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99US-0159331P.
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99US-0159584P.
99US-0160741P.
99US-0160768P.
99US-0160770P.
99US-0160780P.
99US-016081AP.
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86.36%
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79.82%
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Best Local Similarity:
 14-0CT-1999
14-0CT-1999
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18-0CT-1999
21-0CT-1999
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26-0CT-1999
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intron	exon	exon	intron	exon	intron	exon	intron	exon	intron	intron	exon	intron	exon	intron	exon	intron	exon	intron	exon	exon	intron	WO9748793-A1.
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This genomic DNA includes coding exons for a novel C-14 sterol reductase

(see AAW41576) of Arabidopsis thaliana. An Arabidopsis mutant, ell (extra
long life), that displayed a life span that was at least 3 times greater
then wild-type plants, was identified. The ell mutant was isolated by T-
DNA tagging, and used to screen genomic and cDNA libraries from a wild-
type plant to identify the 6588 bp genomic clone and cDNA clone D13 (see
plant to identify the 6588 bp genomic clone and cDNA clone D13 (see
DNA tagging, and used to screen genomic clone and cDNA clone D13 (see
DNA tagging transformed plant cells, a transgenic plant that expresses
C145R bNA and a seed or cell from such a transgenic plant that expresses
C145R bNA and a seed or cell from such a transgenic plant, and methods
C145R in a transgenic plant using an antisense construct. The genetic
manipulation of plant sterol composition is useful for improving food
quality and oil stability, and for regulating the formation of cuapentally increase the life span of plants and produce plants having reduced and
more compact proportions. Overproduction is useful for enhancing the
production of medically or agriculturally useful for enhancing the
character of the compact proportion is useful for enhancing the
character of the compact proportion is useful for enhancing the
character of the compact proportion is useful for enhancing the
character of the compact proportion of the development of enzyme inhibitors of
                                                                                                                                                                                                                                                      of a plant sterol biosynthetic pathway to
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                                                                                                                                                                                                                                                                                                                                                    Claim 28; Fig 15; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides are also useful for
the sterol biosynthetic pathway
                                                                                                                                                                                                                                                 New isolated plant C-14 sterol for the genetic manipulation of improve plant characteristics.
                        96US-0022086P
                                                                     (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                      WPI; 1998-063134/06.
P-PSDB; AAW41576.
                                                                                                                        Sheen J;
                        21-JUN-1996;
                                                                                                                     Jang J,
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22 ValProLeuLeuValGlvPhePheThrTvrLeu-AlaValAlaGlvSerrlleLeuProGl 6588 276 28 44 523 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: US-10-069-427-8 (1-369) x AAV04238 (1-6588) 7,35e-95 990.50 34.98% 31.76% 50.41% Percent Similarity: Best Local Similarity: Query Match: DB: Score: ò g

Alignment Scores:

83		83
3884	TTINGGGAATCTGTGCAAAACTTGGCATTGTATCACCTCTTGTAAGTGTAGTTACAAGAT 3884	3825
83	71 euLeuGly1leGlyAlaLysMetGlyPheValSerPro	71
3824	3765 TITCCATTAGITIGGITAATICAATTTCAGGTCTATTGGCACTAATATTGTTGGTAGCTA 3824	3765
71		61
3764	TATATTTGATTTGATTTACTCTCTCTACAATTCCTGAGAGTCTGTGAGCTCGAAAGTTCA 3764	3705
09		09
3704	GAAAGTTATTGGGGGGTCCTTTTATCAGATGGCTCTCAACTTCGTTACCGATGG 3704	3645
09	41 yLysLeuValProGlyValAlaLeuLeuAspGlyThrArgLeuHisTyrCysCysAsn 60	41
3644	3585 GTTTATGTGCTGGTGTTTTACTTCGTTTACTTGGGNCGNTGGCGGAGAAATTCTCCCCGG 3644	3585
4 T	22 VAIFTODEULEUVALTYFHEFRETITIYIDEU-ALAVALAIASIYSETILEDEUFIGGI 41	77

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97WO-US010644

20-JUN-1997; 24-DEC-1997

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ACTGAGATGTTTGGTAGGTGGTTGCGGATAGAGACTTGAGTTA	117 SerbygGlygerseri 118 4 ATAAGGGTTCTTCC 134	

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LysSerileGlnAspGlyThrLeuSerGlnSerMetIleLeuTyrGlnLeuPheCysAla 185
                              CTGTACATCCTTGATTACTTCTTCTGTGAAGAGTTCATGACCTCCACATGGGATATAATA
                                                                                                                                                        AlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIleProPheSerPhe
                                                                                LeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSerThrTrpAspIleIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention relates to the identification and isolation of novel nucleic acid molecules that confer altered visual phenotypes in plants. Specifically, it refers to modifications of plant architecture and/ or leaf surface features in plants, such as chlorotic, bleaching, etching, wet leaf, stunting, elongation and texture phenotypes, which are thought will be agronomic traits beneficial to the farmer. As such, these novel phenotypes can affect growth regulation i.e. useful for creating dwarf to varieties, exhibit resistance to insects or heat stress, confer changes in planet such that plants have enhanced vitamin production or delayed senescence and also for example produce plants that control the production of ethylene. Furthermore, the present invention comprises production of ethylene. Furthermore, the present invention comprises phenotype of plant seeds, plant tissues and plant cells containing the polymucleotides described herein. This polymucleotide is a homologue of a plant the plants that meaning the plants that containing the plants that meaning an altered visual phenotype when expressed in
6103 TGCAGAGAAGTACNAGGAGATATGGGCAGAGTATCTTAGACTTGTCCCCTGGAGAATACT 6162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryzae
                                                                                                                                                                                                                                                                                                          ds; visual phenotype; plant; architecture; leaf surface; chlorotic; bleaching; etching; wet leaf; stunting; elongation; texture; agronomic trait; growth regulation; dwarf variety; insect resistance;
                                                                                                                                                                                                                                                                     (SeqID 1069) that confers an altered visual phenotype in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid derived from Nicotiana benthamiana, C
sativa, Saccharomyces cerevisiae, and Papaver rhoeas, useful for
conferring altered visual phenotypes in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 625 BP; 165 A; 117 C; 149 G; 194 T; 0 U; 0 Other;
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1069; 517pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ruegger M,
                                                                                                                                                      BP.
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(DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                    ADD17001 standard; DNA; 625
                                                           TCCTTATGTTTAT 6175
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973.00
92.16%
86.27%
                                       uProTyrValTyr 369
                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                        heat stress; transgenic,
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                                                                                                                                                                                             ADD17001;
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GCAGAGAGGTTGGGCTTCATGCTGGTTTTTGGTGATCTAGTCTTATATACCGTTCACCTTC
                                                                                                                                                         GlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsnTyrLeuGlyAsp
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fungicide; expressed sequence tag; EST; ss.
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US-10-069-427-8 (1-369) x ADD17001 (1-625)

Query Match: DB:

ABK35567;

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The present sequence is that of expressed sequence tag clone src3c.pk009.c1, which includes a partial coding region for soybean sterol delta-14 reductase (see AAB20378). The clone was isolated from a cDNA library prepared from soybean 8-day-old root infected with cyst nematode, following database homology searches. The predicted polypeptide shows amino acid sequence homology to Arabidopsis thaliana sterol delta-14 reductase. The invention relates to isolated polymucleotides encoding sterol delta-14 reductases and to transgenic plants comprising such polymucleotides. It also relates to the construction of a chimeric gene encoding all or a portion of the sterol delta-14 reductase, in sense or antisense orientation, where expression of the chimeric gene results in continuous and altered levels of the enzyme in a transformed host cell. The availability of plant sterol delta-14 reductase genes will provide means of altering sterol production and/or composition of plants, to identify compounds that may be useful as novel herbicides and fungicides, and to identify mutants of these genes that are resistant to these herbicides and will enable the production of herbicide-resistant crops
                                                                                                                                             Novel gene encoding sterol delta-14 reductase useful for transgenic plant production with altered sterol delta-14 reductase.
                                                                                                                                                                                                                                   Claim 7; Page 35; 45pp; English
                        Kinney AJ;
                                                                          WPI; 2001-266146/27.
                                                                                                      P-PSDB; AAB20378.
                        Famodu 00,
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Seguence 427 BP; 86 A; 106 C; 95 G; 139 T; 0 U; 1 Other;

Alignment Pred, No.	Scores:	4.21e-66	Length:	427
15 0 E	Similarity: al Similarity: tch:	706.00 100.00% 99.27% 35.93%	Matches: Conservative: Mismatches: Indels: Gaps:	136 1 0 0 0
US-10-069.	-427-8 (1-369)	x AAF30674	(1-427)	
ò	1 MetMetGlu	uSerHisValAspLeuGl	yPheLeuLeuG1	nAlaLeuThrProSerTrpAsn
Db	4 ATGATGGAC	STCACACGTGGATC	raggititcicciicaa	
È	21 SerValPro	roLeuLeuValGlyP	yPhePheThrTyrLeuAla	euAlaValAlaGlySerIleLeuPro
DÞ	64 recerree		CTTACI	TGGCCGTTGCTGGATCCATTCTCCCT
δ	41 GlyLysLet	SLeuValProGlyValAl	arenrenyspglyThr	ArgLeuHisTyrCysCysAsn
ପ୍ରପ	124 GGAAAACTT	CTTGTTCCTGGCGTTG	CACTACTCGATGGAACT	CTCGTCTACACTATTGCTGCAAT
λ̈́o	61 GlyLeuLeu	GlyLeuLeuSerLeuLeuLeuLe	euValAlaLeuLeuGlyIleGlyAl	IleGlyAlaLysMetGlyPhe
QQ	184 GGTCTGCTC	CTCGCTTCTTCTGT	rggrrgcacrrcrcgg	GGTCTGCTCTCGCTTCTTCTGTTGCACTTCTCGGGATCGGTGCCAAGATGGGTTTT
ò	81 ValSerPro	ProThrAlaIleSerA	erAspArgGlyLeuGluLeu	euLeuSerThrThrPheAlaPhe
DÞ	244 GrGrCrcc	CACTGCCATATCAA	acagagacttgagctg	GIGICICCCACIGCCAINICAAACAGAGGACTIGAGCTGCTGCCACAACTITTGCCTTC
ò	101 SerPheLet	erPheLeuValThrLeuIleL	eLeuHisPheSerGlyCys	sLysSerGlnSerLysGlySer
qq	304 AGTTTTCTTGTAACCC	-⊦	GATATTGCATTTTTCCGGGTGC	TCCGGGTGCAGTCACAAGTAAAGGNTCA
δγ	121 SerLeuLys	sProHisLeuSerG	lyAsnLeuIleHisAsp	TrpTrpPheGly 137
qu	364 TCACTAAAG	SCTCATCTCAGTGGGAAC	SGAACCTGATACACGATT	redregringe 414
RESULT 9				

0 m 0 98

LeuLeuValAlaLeuLeuGlyIleGlyAlaLysMetGlyPheValSerProThrAlaIle

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ABK35567 standard; DNA; 3714 BP.

ABK35567 ID ABK

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The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of huan genes or expression products in an endometrial sample suspected of being cancerous. The huan genes of the invention are differentially expressed in breast tumours of characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimes, and identification of compounds useful for the treatment of endometrial cancer, ABRX35531-ABX35581 represent the human genes of the invention that are differentially expressed in breast cancer tissue
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                                                                                         Human, diagnosis of breast cancer, endometrial cancer, breast tumour; MAI; mitotic activity index; cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Diagnosing breast cancer comprises determining expression of nucleic molecules or expression products that are differentially expressed in normal and malignant tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;
                                                             dene LBR differentially expressed in breast cancer tissue.
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(BAAK/) BAAK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 94-96; 219pp; English.
                                                                                                                                                                                                                                              27-JUL-2001; 2001WO-US023642.
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Best Local Similarity:
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Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arbhritis; glomerulonephritis; asthma: thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.

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1102 TATCTCTACATGCGCTCTTTGAAAGCGCCCCGG-----AATGACCTGTCGCCTGCCAGC 1155
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TCTGGAAATGCTGTCTATGATTTCTTCATTGGCGGTGAATTAAACCCTCGAATTGGTACT 1215
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Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 435; 114pp; English.

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Yamaga

SM,

Weissman

WPI; 2002-435328/46. Beazer-Barclay Y,

(GENE-) GENE LOGIC INC.

03-OCT-2001; 2001WO-US030821. 03-OCT-2000; 2000US-0237189P

11-APR-2002

Homo sapiens.

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are medulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in GS; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue or sterile inflammatory disease using the gene expression of pathogen or sterile inflammatory disease using the gene expression of profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression in a subject, exposure of a subject to a pathogen or sterile inflammation of the gene is indicative of inflammation will ammation agent that modulates the expression of gene(s) from Gs, where the level of inflammation wisease, by contacting a tissue having inflammation wisease, by contacting a tissue having inflammation in a tissue, M4 is useful for modulating GA, preferably, in an expension in a tissue, an allergic response in a subject to a pathogen or sterile of inflammation in a tissue, an allergic response in a subject of conscrening an agent capable of modulating GA, preferably, in an expension of gene(s) from Gs in the tissue, M4 is useful for detecting an inflammation of gene(s) cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory disterses sundreme, inflammatory disterses (or incartive, inflammatory disease, confirsue, inflammatory disease, confir did disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fundal infection and MS is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent of the printed specification, but was obtained in electronic format directly from MIPO at the printed specification and the printed specification are obtained in fig. wipo.int/pub/published_pct_sequences

Sequence 3714 BP; 1046 A; 644 C; 759 G; 1265 T; 0 U; 0 Other;

Conservative: 1.31e-56 630.00 55.70% Percent Similarity:

Human cDNA differentially expressed in granulocytic cells #435.

14-AUG-2002

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Alignment Scores:
Pred. No.:
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AAP 30676

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme in a transformed host cell. The availability of plant sterol delta-
14 reductase genes will provide a means of altering sterol production
and/or composition of plants, to identify compounds that may be useful as
novel herbicides and fungicides, and to identify mutants of these genes
that are resistant to these herbicides and will enable the production of
herbicide-resistant crops
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LeuLeulleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIle 352
                                                                                                                                     Soybean, sterol delta-14 reductase, transgenic plant; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Soybean sterol delta-14 reductase clone src3c.pk009.cl:fis.
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                                                                                                                                                                                                                                                                                   334
                                                                                                                                                                                                                                                                                                                             335 IleTrpArgGluArgThrAspGluAlaArgCysAlaGluLysTyrArgGluIleTrpAla 354
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                                                                                                   GlylleAlaArgHisCysAsnTyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeu
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                                                                                                                                                                                              TyrMetValPheArgGlyAlaAsnLysGlnLysHisValPheLysLysAsnProLysAla
                                                                                   235 AsnSerValGluLeuThrProAlaAlaIleValAlaAsnCysPheValPheLeuIleGly
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                                                                                                                                                                                                                                                                                                                                                                            GluTyrargLysLeuValProTrpArgIleLeuProTyrValTyr 369
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20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
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P-PSDB; ABP73823.
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The invention relates to constructing (M1) a strain of diploid fungal cells in which both alleles of a gene are modified, comprising modifying one allele by insertion or replacement by a cassette having an expressible selectable marker and modifying other allele by recombination, of a promoter replacement fragment with a heterologous promoter. (M1) is useful for constructing a strain of diploid fungal cells in which both alleles modified are useful for identifying a gene that contributes to the survival or growth of a fungus, a gene contributes to the virulence and/or pathogenicity of a fungus, a gene contributes to the virulence and/or pathogenicity of a fungus, a gene contributes to the resistance of a diploid fungus to an antifungal agent, an antifungal agent that inhibits the growth of a diploid fungus of and for identifying a therapeutic agent for treatment of a mammalian agent, an antifungal agent that inhibits the growth of a diploid fungus to compound extabolism, biosynthetic, transporter, transcriptional, compound catabolism, biosynthetic, transporter, transcriptional, compound catabolism, signal fransduction, DNA replication and cell division activity, the method is useful for identifying a compound having the ability to inhibit growth or proliferation of C. albicans cells and for trataling infection by C. albicans. The present sequence is that of an essential candida albicans gene used in the method of the invention. Note: The sequence data for this parent is not represented in the printed the burners of the printed t
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GlyAsnLeulleHisAspTrpTrpPheGlyIleGlnLeuAsnProGlnPheMetGlyIle

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-----AlaGlyMetMetGlyTrpLeuLeuIleAsnLeu 161

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δ g ò 셤 SerileLeuMetLysSerileGlnAsp---GlyThrLeuSerGlnSerMetIleLeuTyr 180

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US-10-069-427-8 (1-369) x AAQ89202 (1-2528)
                                                        Disclosure; Page 17; 25pp; English
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WPI; 1995-116992/16.
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Best Local Similarity:
        P-PSDB; AAR71934
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                                                                                                                   241 ProAlaAlaIleValAlaAsnCysPheValPheLeu----IleGlyTyrMetValPhe
                                                                                                                                                                                    LysProProLysVal------IleGlyGlyLysLeuLeuAlaSerGly
                  GlnieuPheCysAlaLeuTyrIleLeuAspTyrPheValHisGluGluTyrMetThrSer
                                                  201 ThrTrpAspileIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrp
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                                                                                                                                                    The S. cerevisiae sterol-delta-14-reductase gene was cloned by selecting strains carrying sequences on a 2-mu vector for resistance to fenpropimorph. Plasmid pMil00 was isolated and shown to carry the structural gene based upon the phenotype of gene disruption strains. The bNA sequence of the 2.5 Sphi/Nabi fragment of pMil00 is given in AA089202 and the encoded 50.5 kDa protein in AAR71934. Over-expression of the DNA in yeast allows assay of inhibitor activity. (Updated on 25-MAR-2003 to
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|GTGTTCAGTTAAGGGATGGTTCGAAGCTTTCGTATAAGATCAATGGAATTGCCATGTCT
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Screening method for sterol delta 14 reductase inhibitors - pref.
comprises binary assay using Neurospora crassa and Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2528 BP; 700 A; 469 C; 507 G; 852 T; 0 U; 0 Other;
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Conservative:
Mismatches:
Indels:
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The present sequence encodes the S. cerevisiae sterol delta-14 reductase, a component of the ergosterol biosynthetic pathway. The sterol delta-14 reductase gene, which was isolated by selecting strains carrying sequences on a 2mu-based to resistance to a morpholine fungicide, e.g. fenpropimorph, or the enzyme can be used in screening tests for the potential fungicides, which may be useful in a wide variety of agricultural, medical and veterinary applications. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                          |||||| ::: |||||| 587 IGGAATCGTACTATCTAGGCAATCGTGAATTATGGACTGTCTAT
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Matches:
Conservative:
Mismatches:
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2mu-based vector; resistance; morpholine; fungicide; fenpropimorph;
screen; identification; biosynthesis; inhibition; agriculture; medicine;
      TrpAspilelleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrplle
                            ATGGATATCACTACAGATGGGTTTGGTTTCATGCTAGCGTTTGGTGACTTTAGTTTAGTTTAGTTTTAGTT
                                                                         242 AlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGlyAla
                                                                                                                          1412 AATAAGCAAAATCTGAGTTTAGACAAGGTAAATTAGAAAATCTAAAAAGTATTCAGACA
                                                                                                                                                                                                              LysvallleGlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsn
                                                                                                                                                                                                                                        1472 AAG---CGTGGTACAAAGTTATTATGTGACGGGTGGGGCTAAATCACAGCATATCAAT
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                                                                                                                                                              AsnLysGlnLysHisValPheLysLysAsnProLysAlaProlleTrpGlyLysProPro
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 TrpAspileIleAlaGluArgLeuGlyPheMetLeuValPheGlyAspLeuValTrpIle 221
                                                                                                      AsnLysGlnLysHisValPheLysLysAsnProLysAlaProlleTrpGlyLysProPro
                                                                                                                    dicacaaatalaaaatatagacaaaaatacaaaaaaaaagattcct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae sterol delta 14 reductase enzyme - useful in
screening for fungicides for agricultural, medical and veterinary
                                                                                      1352 GTGAAAGTTGTCGGTATATTAGCCATAATGTTTTTGGGTTTCCACATCTTCCACTCGGCA
                                                                                                                                                                            TyrLeuGlyAspLeuMetLeuAlaLeuSerPheSerLeuProCysGlylleSerSerPro
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                                                                      242 AlaAlaIleValAlaAsnCysPheValPheLeuIleGlyTyrMetValPheArgGlyAla
                                                                                                                                          LysValileGlyGlyLysLeuLeuAlaSerGlyTyrTrpGlyIleAlaArgHisCysAsn
                                                                                                                                                                                                                IleProTyrPheTyrProIleTyrLeuLeuIleLeuLeuIleTrpArgGluArgThrAsp
                                    PropheSerPheSerIleGlnGlyTrpTrpLeuLeuMetAsnSerValGluLeuThrPro
                                                                                                                                                                                                                                                                                                                                                                                                                   Sterol delta-14 reductase; ergosterol; biosynthetic pathway; identification; sterol biosynthesis; inhibitor; fungicide; ds
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The present sequence encodes S. cerevisiae sterol delta-14 reductase, a member of the ergosterol biosynthetic pathway, which is useful in devising screening tests to identify sterol biosynthesis inhibitors. The inhibitors are potential fungicides which may be used in various agricultural, medical and veterinary applications. The gene was isolated and cloned by selecting strains, carrying sequences on a 2mu based vector, for resistance to a morpholine fungicide, e.g. fenpropimorph. (Updated on 25-MAR-2003 to correct PF field.)
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Matches:
Conservative:
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242 AlaAlaIleValAlaAsnCysPheValPheLeulleGlyTyrMetValPheArgGlyAla 261
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